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(54) Title: DETECTION AND IDENTIFICATION OF HUMAN PAPILLOMAVIRUS BY PCR AND TYPE-SPECIFIC REVERSE HYBRIDIZATION

(57) Abstract

The present invention relates to a method for detection and/or identification of HPV present in a biological sample, comprising the steps of amplification of HPV polynucleic acids and of hybridization of said amplified polynucleic acids to a number of probes. By means of PCR, a short fragment of the L1 gene of HPV is amplified. The amplimers are then contacted with probes that specifically hybridize to said short fragment of the L1 gene of either one or more than one HPV type. A preferred format is the reverse hybridization technique, more particularly the LiPA technique. The invention also relates to primers and probes to be used in a method of detection and/or identification of HPV and to a diagnostic kit to perform said method.

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Detection and identification of Human Papillomavirus by PCR and type-specific reverse hybridization

FIELD OF THE INVENTION

The present invention relates to the field of detection and identification of Human Papillomavirus (HPV) infections in clinical samples.

BACKGROUND OF THE INVENTION

Cervical cancer is the second most common malignancy in women, following breast cancer. Carcinoma of the cervix is unique in that it is the first major solid tumor in which HPV DNA is found in virtually all cases and in precursor lesions worldwide.

Nowadays, 74 HPV genotypes have been characterized and are numbered in chronological order of isolation. HPV is epitheliotropic and infects only the skin (cutaneous types) or the mucosa of the respiratory and anogenital tract (mucosal types). Thirty-six of the 74 HPV types are known to infect the uterine cervix. Based on the induced benign, premalignant or malignant lesions, HPV is divided into low-risk (e.g., HPV types 6, 11, 42, 43 and 44) and high-risk types (e.g., types 16, 18, 31, 33 and 45), respectively. The high-risk types account for more than 80% of all invasive cervical cancers. Consequently, detection and identification of HPV types is very important. The high-risk types are more consistently found in high grade SIL (Squamous Intraepithelial Lesion) and carcinoma in-situ than low-risk types which are mainly found in low grade SIL. This epidemiological observation is supported by molecular findings. For instance, the E6 and E7 proteins from low-risk types 6 and 11 bind p53 and pRB too weakly to immortalize keratinocytes in vitro or to induce malignant transformation in vivo (Woodworth et al., 1990). The circular ds-DNA genome of low-risk HPV types remains episomal whereas the genome of high-risk HPV types is able to integrate into the human genome.

Screening for malignant and premalignant disorders of the cervix is usually performed according to the Papanicoloau (PAP) system. The cervical smears are examined by light

microscopy and the specimens containing morphologically abnormal cells are classified into PAP I to V, at a scale of increasing severity of the lesion. This cytomorphological method is an indirect method and measures the possible outcome of an HPV infection. Therefore, HPV DNA detection and typing is of importance in secondary screening in order to select patients for monitoring (follow-up) and treatment. This means that cervical smears classified as PAP II (atypical squamous metaplasia) or higher classes should be analyzed for low-risk and high-risk HPV types. Follow-up studies have shown that only high-risk HPV types are involved in the progression from cytologically normal cervix cells to high grade SIL (Remminck et al., 1995). These results indicate that the presence of high-risk HPV types is a prognostic marker for development and detection of cervical cancer.

Detection of HPV infections

Diagnosis of HPV by culture is not possible. Also diagnosis by detection of HPV antibodies appears to be hampered by insufficient sensitivity and specificity. Direct methods to diagnose an HPV infection are mainly based on detection of the viral DNA genome by different formats of DNA/DNA hybridization with or without prior amplification of HPV DNA. The polymerase chain reaction (PCR) is a method that is highly efficient for amplification of minute amounts of target DNA. Nowadays, mainly three different primer pairs are used for universal amplification of HPV DNA. Two of these primer pairs, MY11/MY09 and GP5/GP6, are directed to conserved regions among diffent HPV types in the L1 region (Manos et al., 1989; Van den Brule et al., 1990). The other primer pair, CPI/CPIIg, is directed to conserved regions in the E1 region (Tieben et al., 1993).

Typing of HPV isolates

There are several methods to identify the various HPV types.

1. HPV DNA can be typed by PCR primers that recognize only one specific type. This method is known as type-specific PCR. Such methods have been described for HPV types 6, 11, 16, 18, 31 and 33 (Claas et al., 1989; Cornelissen et al., 1989; Falcinelli et al., 1992; Van den Brule et al., 1990; Young et al., 1989). The primers are aimed at the E5, L1, E6, L1, E2 and E1 regions of the HPV genome for types 6, 11, 16, 18, 31 and 33, respectively (Baay et al., 1996). The synthesized amplimer sizes vary from 217 bp to 514 bp.

2. Another method is general amplification of a genomic part from all HPV types followed by hybridization with two cocktails of type-specific probes differentiating between the oncogenic and non-oncogenic groups, respectively. A similar typing method has been described without prior amplification of HPV DNA. In the Hybrid capture assay (Hybrid Capture Sharp Assay; Digene, Silver Springs, MD), each sample is tested for a group of "high-risk" HPV types (16, 18, 31, 33, 35, 45, 51, 52 and 56) and for another group of "low-risk" HPV types (6, 11, 42, 43 and 44) (Cox et al., 1995).

At present, classification of human papillomaviruses can be performed for instance by sequence analysis of a 450 bp PCR fragment synthesized by the primers MY11/MY09 in the L1 region (Chan et al., 1995) or by the primers CPI and CPIIg in the E1 region (Tieben et al., 1993). Phylogenetic analysis of these sequences allows classification of the different HPV types. By definition, if the sequence differences between two HPV isolates is higher than 10% they are classified as different types. Consequently, if the sequence differs more than 10% from any known HPV type it is classified as a novel HPV genotype. HPV isolates that differ between 2-10% are classified as different subtypes. Finally, if the sequence variation is below 2%, the 2 isolates are classified within the same subtype as different variants.

AIMS OF THE INVENTION

It is an aim of the present invention to provide a rapid and reliable method for detection and/or identification of HPV, possibly present in a biological sample.

It is more particularly an aim of the present invention to provide a method for detection and/or identification of HPV comprising amplification of a polynucleic acid fragment of HPV and subsequent hybridization of this fragment to suitable probes.

It is also an aim of the present invention to provide a number of oligonucleotide primers and probes enabling said method of detection and/or amplification of HPV.

It is also an aim of the present invention to provide new HPV sequences.

It is furthermore an aim of the present invention to provide protocols according to which said amplification and hybridization steps can be performed. One format for the hybridization step is, for instance, the reverse hybridization format, and more particularly the

LiPA technique.

It is also an aim of the present invention to compose diagnostic kits comprising said primers and probes, permitting the rapid and reliable detection and/or identification of HPV possibly present in a biological sample.

All the aims of the present invention are met by the following specific embodiments.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a method for detection and/or identification of HPV, possibly present in a biological sample, comprising the following steps:

(i) amplification of a polynucleic acid fragment of HPV by use of:

-a 5'-primer specifically hybridizing to the A region or B region of the genome of at least one HPV type, said A region and B region being indicated in figure 1, and

-a 3'-primer specifically hybridizing to the C region of the genome of at least one HPV type, said C region being indicated in figure 1;

(ii) hybridizing the amplified fragments from step (i) with at least one probe capable of specific hybridization with the D region of at least one HPV type, said D region being indicated in figure 1.

According to one preferred embodiment of the present invention, said probe mentioned in step (ii) is capable of specific hybridization with the D region of the genome of only one HPV type, and thus enables specific identification of this HPV type, when this type is present in a biological sample.

According to another preferred embodiment of the present invention, said probe mentioned in step (ii) is capable of specific hybridization with the D region of more than one HPV type, and thus enables detection of any of said more than one HPV type, when any of said types is present in a biological sample.

According to another preferred embodiment of the present invention, the 3'-end of said 5'-primer specifically hybridizing to the A region of the genome of at least one HPV type, is situated at position 6572 of the genome of HPV 16, or at the corresponding position

of any other HPV genome, as indicated in figure 1.

According to another preferred embodiment of the present invention, the 3'-end of said 5'-primer specifically hybridizing to the B region of the genome of at least one HPV type, is situated at position 6601 of the genome of HPV 16, or at the corresponding position of any other HPV genome, as indicated in figure 1.

According to another preferred embodiment of the present invention, the 3'-end of said 3'-primer specifically hybridizing to the C region of the genome of at least one HPV type, is situated at position 6624 of the genome of HPV 16, or at the corresponding position of any other HPV genome, as indicated in figure 1.

According to another preferred embodiment of the present invention, said probe capable of specific hybridization with the D region of the genome of only one HPV type, more particularly specifically hybridizes to the E region, with said E region being a subregion of the D region, as indicated in figure 1.

According to another preferred embodiment of the present invention, said probe capable of specific hybridization with the D region of the genome of only one HPV type, more particularly specifically hybridizes to the 22 bp region situated between the B region and the C region, as indicated in figure 1.

According to another preferred embodiment, said 5'-primer specifically hybridizing to the A region of the genome of at least one HPV type, is chosen from the following list:

SGP3, SGP3A, SGP3B, SGP3C, SGP3D, SGP3E, SGP3F, SGP3G.

The sequences of said primers are shown in table 1 and in table 4.

According to another preferred embodiment, said 5'-primer specifically hybridizing to the B region of the genome of at least one HPV type, is chosen from the following list:

SGP1, SGP1A, SGP1B, SGP1C, SGP1D.

The sequences of said primers are shown in table 1, in table 4 and in table 11.

According to another preferred embodiment, said 3'-primer specifically hybridizing to the C region of the genome of at least one HPV type, is chosen from the following list:

SGP2, SGP2A, SGP2B, SGP2C, SGP2D, SGP2E, SGP2F, SGP2H, SGP2I, SGP2J, SGP2K, SGP2L, SGP2M, SGP2N, SGP2P.

The sequences of said primers are shown in table 1, in table 4 and in table 11.

According to another preferred embodiment, said probe capable of specific hybridization with the aforementioned 22bp region of only one HPV type, is chosen from the following list:

HPV6 Pr1, HPV6 Pr2, HPV6 Pr3, HPV6 Pr4, HPV6 Pr5, HPV11 Pr1, HPV11 Pr2, HPV11 Pr3, HPV11 Pr4, HPV11 Pr5, HPV16 Pr1, HPV16 Pr2, HPV16 Pr3, HPV16 Pr4, HPV16 Pr5, HPV18 Pr1, HPV18 Pr2, HPV18 Pr3, HPV18 Pr4, HPV18 Pr5, HPV31 Pr1, HPV31 Pr2, HPV31 Pr3, HPV31 Pr4, HPV31 Pr5, HPV31 Pr21, HPV31 Pr22, HPV31 Pr23, HPV31 Pr24, HPV31 Pr25, HPV31 Pr26, HPV31 Pr31, HPV31 Pr32, HPV33 Pr1, HPV33 Pr2, HPV33 Pr3, HPV33 Pr4, HPV33 Pr5, HPV33 Pr21, HPV33 Pr22, HPV33 Pr23, HPV33 Pr24, HPV33 Pr25, HPV33 Pr26, HPV40 Pr1, HPV45 Pr1 (= SGPP68), HPV45 Pr2, HPV45 Pr3, HPV45 Pr4, HPV45 Pr5, HPV45 Pr11, HPV45 Pr12, HPV45 Pr13, HPV52 Pr1, HPV52 Pr2, HPV52 Pr3, HPV52 Pr4, HPV52 Pr5, HPV52 Pr6, HPV56 Pr1, HPV56 Pr2, HPV56 Pr3, HPV56 Pr11, HPV56 Pr12, HPV58 Pr1, HPV58 Pr2, HPV58 Pr3, HPV58 Pr4, SGPP35, SGPP39, SGPP51 (= HPV51 Pr1), SGPP54, SGPP59, SGPP66, SGPP70 (= HPV70 Pr11), SGPP13, SGPP34, SGPP42, SGPP43, SGPP44, SGPP53, SGPP55, SGPP69, SGPP61, SGPP62, SGPP64, SGPP67, SGPP74 (= HPV74 Pr13), MM4 (= HPVM4 Pr11), MM7, MM8, HPV18b Pr1, HPV18b Pr2, HPV31 Vs40-1, HPV31 Vs40-2, HPV31 Vs40-3, HPV34 Pr1, HPV35 Pr1, HPV35 Pr2, HPV35 Pr3, HPV39 Pr1, HPV42 Pr1, HPV42 Pr2, HPV43 Pr1, HPV43 Pr2, HPV43 Pr3, HPV44 Pr1, HPV44 Pr2, HPV44 Pr3, HPV44 Pr4, HPV45 Pr5, HPV51 Pr2, HPV53 Pr1, HPV54 Pr1, HPV54 Pr11, HPV54 Pr11as, HPV54 Pr12, HPV55 Pr1, HPV55 Pr11, HPV55 Pr12, HPV55 Pr13, HPV56 Vs74-1, HPV59 Pr1, HPV59 Pr11, HPV59 Pr12, HPV59 Pr13, HPV66 Pr1, HPV67 Pr1, HPV 67Pr11, HPV67 Pr12, HPV67 Pr13, HPV67 Pr21, HPV67 Pr22, HPV67 Pr23, HPV68 Pr1, HPV68 Pr2,HPV68 Pr3, HPV68 Vs45-1, HPV68 Vs45-2, HPV70 Pr1, HPV70 Pr12, HPV70 Pr13, HPV74 Pr1, HPV74 Pr11, HPV74 Pr12, HPV74 Pr2, HPV74 Pr3, HPVM4 Pr1, HPVM4 Pr12, HPVM4 Pr21, HPVM4 Pr22.

The sequences of said probes are shown in table 7 and table 12.

It is to be understood that combinations of the aforementioned embodiments are also preferred embodiments, for instance a method characterized in that said 5'-primer specifically hybridizing to the A region is chosen from the aforementioned respective list and that said 3'-

primer specifically hybridizing to the C region is chosen from the aforementioned respective list.

It is an important feature of the present invention that the amplified polynucleic acid fragments of HPV fall within a short region of the L1 gene, a region that presents a high degree of sequence variability. Said region is denoted D region and for any HPV type consists of the region corresponding in a sequence alignment to the region from position 6553 to position 6646 of the genome of HPV 16, with the numbering being according to isolate PPH16, with Genbank accession number K02718. The advantage of amplifying a short fragment is that higher sensitivity can be obtained, i.e. a lower number of copies of HPV polynucleic acids can be detected and/or identified. The aforementioned primers may be used to amplify a fragment of approximately 65 bp (by use of 5'-primers specifically hybridizing to the B region and 3'-primers specifically hybridizing to the C region) or a fragment of approximately 94 bp (by use of 5'-primers specifically hybridizing to the A region and 3'-primers specifically hybridizing to the C region). However, it is obvious to one skilled in the art that other primers may be used in order to amplify other fragments within or overlapping with said D region. Preferred primers are shown in table 1 and in table 4. These primers permit amplification of polynucleic acid fragments of a large group of HPV types, but it may be desirable for some purposes to chose primers that selectively amplify a smaller group of HPV types.

The different types of HPV in a sample can be identified by hybridization of polynucleic acids of said types of HPV to at least one, preferably at least two, more preferably at least three, even more preferably at least four and most preferably at least five oligonucleotide probes. These probes may be designed to specifically hybridize to the D region of only one HPV genome, said D region being indicated in figure 1. Tables 7 and 12 contain a list of preferred probes specifically hybridizing to the 22 bp region within said D region, situated between the B region and the C region. These probes may be used together under the same conditions of hybridization and washing, for instance in a LiPA format (see below). Probes that have been optimized to work together in a LiPA format are for instance the combination of HPV6 Pr1, HPV11 Pr1, HPV16 Pr1, HPV18 Pr1, HPV31 Pr25, HPV31 Pr31, HPV31 Pr32, HPV33 Pr21, HPV33 Pr25, HPV40 Pr1, HPV45 Pr11, HPV45 Pr12, HPV45 Pr13, HPV52 Pr5, HPV52 Pr6, HPV56 Pr11, HPV56 Pr12, HPV58 Pr2, HPV58 Pr3

and HPV58 Pr4 (see example 4), the combination of HPV6 Pr1, HPV11 Pr5, HPV16 Pr1, HPV18 Pr1, HPV18b Pr2, HPV31 Pr31, c31-3, HPV33 Pr21, HPV34 Pr1, HPV35 Pr1,HPV39 Pr1, HPV40 Pr1, HPV42 Pr1, HPV43 Pr3, HPV44 Pr1, HPV45 Pr11, HPV51 Pr2, HPV52 Pr5, HPV53 Pr1, HPV56 Pr12, c56-1, HPV58 Pr2, HPV59 Pr12, HPV66 Pr1, HPV68 Pr1,c68-1, HPV70 Pr12 and HPV74 Pr1, or the combination outlined in example 7. Probes specifically hybridizing to said 22 bp region should permit discrimination of all genital low-risk types including HPV types 6, 11, 34, 40, 42-44, 53, 54, 55, 59, 61, 62, 64, 67, 68, 71 and 74 as well as all genital high-risk types including HPV types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56-58, 66 and 69 (zur Hausen, 1996). It should be clear to one skilled in the art that other probes than those listed in table 7 or 12 may be chosen within said region D, provided that they specifically hybridize to only one HPV-type. It should also be clear that in some cases probes may be chosen that overlap with the primers used in the amplification step. In this case, however, the region of overlap between primer and probe should not be as long as to allow by itself duplex formation under the experimental conditions used. It should furthermore be clear that, if presently unknown types are detected that differ in the D region from all presently known types, the methods of this invention will also enable detection and/or identification of said presently unknown HPV types. The present invention furthermore discloses novel sequences in said 22 bp region, as shown in example 5 and in figure 1 (SEQ ID NO 135-153). Probes or primers that are designed to specifically hybridize to these sequences, may be used in a method to detect and/or to identify HPV polynucleic acids comprising any of these sequences, when these polynucleic acids are present in a biological sample.

According to another preferred embodiment of the present invention, probes are used that specifically hybridize to the D region, or more particularly to the E region of more than one HPV type. Examples of such probes are given in table 9 and in table 10. The probes in table 9 have been designed for hybridization in a microtiter plate, e.g. according to the DEIA technique (see below), whereas the probes in table 10 are more suitable for the LiPA technique (see below). These probes hybridize to the E region of more than one HPV type, and hence may be used to detect the presence in a biological sample of any of the types to which they hybridize. It should be clear to one skilled in the art that, according to this embodiment, other probes than those listed in table 9 and table 10 may be chosen within the

D region, provided that they hybridize to one or more than one HPV type.

According to another preferred embodiment of the present invention, the aforementioned methods of detection and/or identification of HPV are characterized further in that the hybridization step involves a reverse hybridization format. This format implies that the probes are immobilized to certain locations on a solid support and that the amplified HPV polynucleic acids are labelled in order to enable the detection of the hybrids formed. According to this embodiment, at least one probe, or a set of a least 2, preferably at least 3, more preferably at least 4 and most preferably at least 5 probes is used. When at least 2 probes are used, said probes are meticulously designed in such a way that they specifically hybridize to their target sequences under the same hybridization and wash conditions.

According to an even more preferred embodiment of the present invention, the aforementioned hybridization step is performed according to the LiPA technique. Said technique involves a reverse hybridization assay, characterized in that the oligonucleotide probes are immobilized on a solid support as parallel lines (Stuyver et al., 1993; international application WO 94/12670). The reverse hybridization format and particularly the LiPA format have many practical advantages as compared to other DNA techniques or hybridization formats, especially when the use of a combination of probes is preferable or unavoidable to obtain the relevant information sought.

Alternatively, detection of HPV polynucleic acids in a biological sample may be performed by use of the DNA Enzyme Immuno Assay (DEIA). This method is used for rapid and specific detection of PCR products. PCR products are generated by a primer set, of which either the forward or the reverse primer contain biotin at the 5' end. This allows binding of the biotinylated amplimers to streptavidin-coated microtiter wells. PCR products are denatured by sodium hydroxide, which allows removal of the non-biotinylated strand. Specific labelled oligonucleotide probes (e.g. with digoxigenin) are hybridized to the single-stranded immobilized PCR product and hybrids are detected by enzyme-labelled conjugate and colorimetric methods.

The present invention also relates to sets of oligonucleotides, said sets comprising at least one primer and/or at least one probe that may be used to perform the methods for detection and/or identification of HPV as described above. Preferred primers according to the present invention can for instance be chosen from table 1, table 4 and table 11. Preferred

probes are shown in tables 7, 9, 10 and 12. These probes can be optimized to be used together in a given format, e.g. a LiPA format, under the same hybridization and washing conditions. Evidently, when other hybridization conditions would be preferred, all probes should be adapted accordingly by adding or deleting one or more nucleotides at their extremities. It should be understood that these concomitant adaptations should give rise to the same result, namely that the probes still hybridize specifically to their respective type-specific target sequences. Such adaptations may also be necessary if the amplified material is RNA and not DNA as is the case in the NASBA system.

The present invention also relates to diagnostic kits for detection and/or identification of HPV, possibly present in a biological sample, comprising the following components:

(i) at least one suitable primer or at least one suitable primer pair;

(ii) at least one suitable probe, preferably at least 2, more preferably at least 3, even more preferably at least 4 and most preferably at least 5 suitable probes, possibly fixed to a solid support;

(iii) a hybridization buffer, or components necessary for the production of said buffer, or instructions to prepare said buffer;

(iv) a wash solution, or components necessary for the production of said solution, or instructions to prepare said solution;

(v) optionally a means for detection of the hybrids formed;

(vi) optionally a means for attaching the probe(s) to a known location on a solid support.

The following definitions and explanations will permit a better understanding of the present invention.

HPV isolates that display a sequence difference of more than 10% to any previously known type in the combined nucleotide sequences of E6, E7 and L1 genes (Chan et al., 1995, de Villiers, 1994) are classified as different HPV "genotypes". HPV isolates that differ between 2 and 10% are classified as different "subtypes". If the sequence variation is below 2%, the isolates are classified within the same subtype as different "variants". The term "type" when applied to HPV refers to any of the three categories defined above.

The target material in the samples to be analyzed may either be DNA or RNA, e.g. genomic DNA, messenger RNA, viral RNA or amplified versions thereof. These molecules are in this application also termed "polynucleic acids".

Well-known extraction and purification procedures are available for the isolation of RNA or DNA from a sample (e.g. in Sambrook et al.,1989).

The term "probe" according to the present invention refers to a single-stranded oligonucleotide which is designed to specifically hybridize to HPV polynucleic acids.

The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides long. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions at which the primer is used, such as temperature and ionic strength.

The expression "suitable primer pair" in this invention refers to a pair of primers allowing the amplification of part or all of the HPV polynucleic acid fragment for which probes are immobilized.

The term "target sequence" of a probe or a primer according to the present invention is a sequence within the HPV polynucleic acids to which the probe or the primer is completely complementary or partially complementary (i.e. with some degree of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases. Probes of the present invention should be complementary to at least the central part of their target sequence. In most cases the probes are completely complementary to their target sequence. The term "type-specific target sequence" refers to a target sequence within the polynucleic acids of a given HPV type that contains at least one nucleotide difference as compared to any other HPV-type.

"Specific hybridization" of a probe to a region of the HPV polynucleic acids means that, after the amplification step, said probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions said probe does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It should be understood that probes that are designed for specific hybridization to a region of HPV polynucleic acids, may fall within said region or may to a large extent overlap with said region (i.e. form a duplex with nucleotides outside as well as within said region). For instance, some of the probes that are shown in table 7 and that are

designed for specific hybridization to the 22 bp region between the B and the C regions (figure 1), extend up to 5 nucleotides beyond the 3'-end of said 22 bp region and other probes of table 7 extend up to 3 nucleotides beyond the 5'-end of said 22 bp region.

"Specific hybridization" of a primer to a region of the HPV polynucleic acids means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions said primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It should be understood that primers that are designed for specific hybridization to a region of HPV polynucleic acids, may fall within said region or may to a large extent overlap with said region (i.e. form a duplex with nucleotides outside as well as within said region).

Since the current application requires the detection of single base pair mismatches, stringent conditions for hybridization of probes are required, allowing only hybridization of exactly complementary sequences. However, it should be noted that, since the central part of the probe is essential for its hybridization characteristics, possible deviations of the probe sequence versus the target sequence may be allowable towards the extremities of the probe when longer probe sequences are used. Variations are possible in the length of the probes. Said deviations and variations, which may be conceived from the common knowledge in the art, should however always be evaluated experimentally, in order to check if they result in equivalent hybridization characteristics as the exactly complementary probes.

Preferably, the probes of the invention are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides. Particularly preferred lengths of probes include 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics.

Probe sequences are represented throughout the specification as single stranded DNA oligonucleotides from the 5' to the 3' end. It is obvious to the man skilled in the art that any of the below-specified probes can be used as such, or in their complementary form, or in their RNA form (wherein T is replaced by U).

The probes according to the invention can be prepared by cloning of recombinant

plasmids containing inserts including the corresponding nucleotide sequences, if need be by excision of the latter from the cloned plasmids by use of the adequate nucleases and recovering them, e.g. by fractionation according to molecular weight. The probes according to the present invention can also be synthesized chemically, for instance by the conventional phospho-triester method.

The fact that amplification primers do not have to match exactly with the corresponding target sequence in the template to warrant proper amplification is amply documented in the literature (Kwok et al., 1990). However, when the primers are not completely complementary to their target sequence, it should be taken into account that the amplified fragments will have the sequence of the primers and not of the target sequence. Primers may be labelled with a label of choice (e.g. biotine). The amplification method used can be either polymerase chain reaction (PCR; Saiki et al., 1988), ligase chain reaction (LCR; Landgren et al., 1988; Wu & Wallace, 1989; Barany, 1991), nucleic acid sequence-based amplification (NASBA; Guatelli et al., 1990; Compton, 1991), transcription-based amplification system (TAS; Kwoh et al., 1989), strand displacement amplification (SDA; Duck, 1990; Walker et al., 1992) or amplification by means of Qß replicase (Lizardi et al., 1988; Lomeli et al., 1989) or any other suitable method to amplify nucleic acid molecules known in the art.

The oligonucleotides used as primers or probes may also comprise nucleotide analogues such as phosphorothiates (Matsukura et al., 1987), alkylphosphorothiates (Miller et al., 1979) or peptide nucleic acids (Nielsen et al., 1991; Nielsen et al., 1993) or may contain intercalating agents (Asseline et al., 1984). As most other variations or modifications introduced into the original DNA sequences of the invention these variations will necessitate adaptions with respect to the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However the eventual results of hybridization will be essentially the same as those obtained with the unmodified oligonucleotides. The introduction of these modifications may be advantageous in order to positively influence characteristics such as hybridization kinetics, reversibility of the hybrid-formation, biological stability of the oligonucleotide molecules, etc.

The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the

background level of hybridization remains low. Usually the solid substrate will be a microtiter plate (e.g. in the DEIA technique), a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead) or a chip. Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic groups, NH_2 groups, SH groups, carboxylic groups, or coupling with biotin, haptens or proteins.

The term "labelled" refers to the use of labelled nucleic acids. Labelling may be carried out by the use of labelled nucleotides incorporated during the polymerase step of the amplification such as illustrated by Saiki et al. (1988) or Bej et al. (1990) or labelled primers, or by any other method known to the person skilled in the art. The nature of the label may be isotopic (^{32}P, ^{35}S, etc.) or non-isotopic (biotin, digoxigenin, etc.).

The "sample" may be any biological material taken either directly from the infected human being (or animal), or after culturing (enrichment). Biological material may be e.g. scrapes or biopsies from the urogenital tract or any part of the human or animal body.

The sets of probes of the present invention will include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more probes. Said probes may be applied in two or more (possibly as many as there are probes) distinct and known positions on a solid substrate. Often it is preferable to apply two or more probes together in one and the same position of said solid support.

For designing probes with desired characteristics, the following useful guidelines known to the person skilled in the art can be applied.

Because the extent and specificity of hybridization reactions such as those described herein are affected by a number of factors, manipulation of one or more of those factors will determine the exact sensitivity and specificity of a particular probe, whether perfectly complementary to its target or not. The importance and effect of various assay conditions are explained further herein.

**The stability of the [probe : target] nucleic acid hybrid should be chosen to be compatible with the assay conditions. This may be accomplished by avoiding long AT-rich sequences, by terminating the hybrids with G:C base pairs, and by designing the probe with an appropriate Tm. The beginning and end points of the probe should be chosen so that the

length and %GC result in a Tm about 2-10°C higher than the temperature at which the final assay will be performed. The base composition of the probe is significant because G-C base pairs exhibit greater thermal stability as compared to A-T base pairs due to additional hydrogen bonding. Thus, hybridization involving complementary nucleic acids of higher G-C content will be more stable at higher temperatures.

**Conditions such as ionic strength and incubation temperature under which a probe will be used should also be taken into account when designing a probe. It is known that the degree of hybridization will increase as the ionic strength of the reaction mixture increases, and that the thermal stability of the hybrids will increase with increasing ionic strength. On the other hand, chemical reagents, such as formamide, urea, DMSO and alcohols, which disrupt hydrogen bonds, will increase the stringency of hybridization. Destabilization of the hydrogen bonds by such reagents can greatly reduce the Tm. In general, optimal hybridization for synthetic oligonucleotide probes of about 10-50 bases in length occurs approximately 5°C below the melting temperature for a given duplex. Incubation at temperatures below the optimum may allow mismatched base sequences to hybridize and can therefore result in reduced specificity.

**It is desirable to have probes which hybridize only under conditions of high stringency. Under high stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. The degree of stringency is chosen such as to maximize the difference in stability between the hybrid formed with the target and the nontarget nucleic acid. In the present case, single base pair changes need to be detected, which requires conditions of very high stringency.

**The length of the probe sequence can also be important. In some cases, there may be several sequences from a particular region, varying in location and length, which will yield probes with the desired hybridization characteristics. In other cases, one sequence may be significantly better than another which differs merely by a single base. While it is possible for nucleic acids that are not perfectly complementary to hybridize, the longest stretch of perfectly complementary base sequence will normally primarily determine hybrid stability. While oligonucleotide probes of different lengths and base composition may be used,

preferred oligonucleotide probes of this invention are between about 5 to 50 (more particularly 10-25) bases in length and have a sufficient stretch in the sequence which is perfectly complementary to the target nucleic acid sequence.

**Regions in the target DNA or RNA which are known to form strong internal structures inhibitory to hybridization are less preferred. Likewise, probes with extensive self-complementarity should be avoided. As explained above, hybridization is the association of two single strands of complementary nucleic acids to form a hydrogen bonded double strand. It is implicit that if one of the two strands is wholly or partially involved in a hybrid that it will be less able to participate in formation of a new hybrid. There can be intramolecular and intermolecular hybrids formed within the molecules of one type of probe if there is sufficient self complementarity. Such structures can be avoided through careful probe design. By designing a probe so that a substantial portion of the sequence of interest is single stranded, the rate and extent of hybridization may be greatly increased. Computer programs are available to search for this type of interaction. However, in certain instances, it may not be possible to avoid this type of interaction.

**Standard hybridization and wash conditions are disclosed in the Materials & Methods section of the Examples. Other conditions are for instance 3X SSC (Sodium Saline Citrate), 20% deionized FA (Formamide) at 50°C. Other solutions (SSPE (Sodium saline phosphate EDTA), TMAC (Tetramethyl ammonium Chloride), etc.) and temperatures can also be used provided that the specificity and sensitivity of the probes is maintained. When needed, slight modifications of the probes in length or in sequence have to be carried out to maintain the specificity and sensitivity required under the given circumstances.

In order to identify different HPV types with the selected set of oligonucleotide probes, any hybridization method known in the art can be used (conventional dot-blot, Southern blot, sandwich, etc.). However, in order to obtain fast and easy results if a multitude of probes are involved, a reverse hybridization format may be most convenient. In a preferred embodiment the selected probes are immobilized to a solid support in known distinct locations (dots, lines or other figures). In another preferred embodiment the selected set of probes are immobilized to a membrane strip in a line fashion. Said probes may be immobilized individually or as mixtures to delineated locations on the solid support. A specific and very user-friendly embodiment of the above-mentioned preferential method is

the LiPA method, where the above-mentioned set of probes is immobilized in parallel lines on a membrane, as further described in Example 4. The HPV polynucleic acids can be labelled with biotine, and the hybrid can then, via a biotine-streptavidine coupling, be detected with a non-radioactive colour developing system.

The term "hybridization buffer" means a buffer allowing a hybridization reaction between the probes and the polynucleic acids present in the sample, or the amplified products, under the appropriate stringency conditions.

The term "wash solution" means a solution enabling washing of the hybrids formed under the appropriate stringency conditions.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of stated integers or steps but not to the exclusion of any other integer or step or group of integers or steps.

FIGURE AND TABLE LEGENDS

Figure 1. Alignment of HPV sequences

Alignment of sequences of genital HPV types and previously unknown sequences within the region from position 6553 to position 6646 (numbered according to HPV 16, Genbank locus name PPH16, accession number K02718), denoted region D. Hyphens indicate the presence of identical nucleotides as in HPV 16. The primer target regions A, B and C are boxed. The sequences identified as 95M or 97M followed by a number are novel sequences disclosed by the present invention. The SEQ ID NO of the novel squences is shown between brackets.

Figure 2. Outline of the HPV DNA genome

Schematic outline of the HPV genome. The Early (E) and Late (L) antigens are boxed. The length of the amplimers that can be synthesized by the different general primer sets in the L1 region is shown by a horizontal bar (bp stands for base pairs).

Figure 3. Phylogenetic tree of HPV sequences in the MY11/MY09 region

Phylogenetic analyses were performed with the Phylip 3.5c software (Felsenstein, 1995). The numbers correspond to the different HPV types; the HPV groups are also indicated.

Figure 4. Phylogenetic tree of HPV sequences between regions B and C.

Phylogenetic analyses of the region between B and C (corresponding to position 6602 to 6623 of HPV 16) were performed with the Phylip 3.5c software (Felsenstein, 1995). The numbers correspond to the HPV types.

Figure 5. Phylogenetic tree of HPV sequences between regions A and C.

Phylogenetic analyses of the region between A and C (corresponding to position 6573 to 6623 of HPV 16) were performed with the Phylip 3.5c software (Felsenstein, 1995). The numbers correspond to the HPV types.

Figure 6. Outline of a HPV LiPA

The bottom panel shows a possible configuration of a LiPA strip enabling detection and identification of HPV types 16, 18, 31, 33, 45, 6 and 11 (ook 52, 56, 58, 40?). The lines correspond to the positions of type-specific probes. "Control" indicates the position of biotinlyated DNA that is used as a control for the conjugate and substrate reaction. "General HPV" indicates the position of probes that enable detection of almost all HPV types. For the amplification step, primers SGP1 and SGP2 can be used; the position of these primers is indicated in the top panel.

Figure 7. LiPA experiment

Plasmids containing complete genomic sequences from the HPV types 6, 11, 16, 18, 31, 33 and 45 were subjected to PCR with primer set SGP1-bio/SGP2-bio. Subsequently, the

amplimers were analysed in a LiPA assay containing type-specific probes for recognition of the HPV types 6, 11, 16, 18, 31, 33 and 45. The strips A and B contained 5 probes for each of these types, as indicated. Of each probe, two amounts (0.2 and 1 pmol) were present on the strip. The probes for recognition of types 6, 11, 16 and 18 were applied to strip A and those for types 31, 33 and 45 were applied to strip B.

Figure 8. LiPA experiment

Amplimers synthesized by use of primer set SGP1-bio/MY09-bio from HPV types 6, 16, 31, 33 and 45 were analysed by means of a LiPA experiment. The strip contained 5 probes for each of the types; of each probe two amounts were present. Strip A contains the probes for recognition of types 6, 11, 16 and 18, whereas strip B contains the probes for types 31, 33 and 45.

Figure 9. Nucleotide sequence alignments of 39 HPV genotypes

Alignment of HPV sequences within the region from position 6582 to position 6646 (numbered according to HPV 16, GenBank locus name PPH16, accession number K02718). Hyphens indicate the presence of identical nucleotides as in HPV 16. The primer target regions B and C are boxed.

Figure 10. Outline HPV-LiPA for identification of 25 types

The LiPA strip shows a possible configuration enabling detection and identification of HPV types 6, 11, 16, 18, 31, 33, 34, 35, 39, 40, 42, 43, 44, 45, 51, 52, 53, 54, 56, 58, 59, 66, 68, 70 and 74. The lines correspond to the positions of type-specific probes. "Control" indicates the position of biotinylated DNA that is used as a control for the conjugate and substrate reaction.

Figure 11. Typical HPV-LiPA patterns

Plasmids containing genomic sequences of HPV genotypes 6, 11, 16, 18, 33, 35, 45, 51, 52,

53, 56, 59, 66, 68, and 70 were subjected to PCR using primers directed to the B and C region in figure 9. Subsequently, the amplimers were analysed in a LiPA experiment containing type-specific probes for identification of 25 HPV genotypes. The colored bands indicate hybridization of the amplimer to the type-specific probe.

Table 1. HPV L1 primers for the A, B and C regions

Selection of preferred primers specifically hybridizing to the A, B or C regions. HPV16, MY16s and SGP16as represent the corresponding sequence of HPV type 16. MY11 was described by Manos et al. (1989). A + sign indicates that the primer is a sense (forward) primer; a - sign refers to an antisense (reverse) primer.

Table 2. HPV DNA detection by the novel general primers SGP1/SGP2.

Plasmids containing HPV polynucleic acids were subjected to PCR with primer sets SGP1/SGP2 and SGP3/GP6. + indicates that an amplimer was obtained. - indicates that no amplimer was obtained. n.d. indicates that this HPV plasmid was not subjected to PCR with the SGP3/GP6 primer set. An amplimer was obtained for all HPV plasmids with the SGP1/SGP2 primer set, although the amount of PCR-product was different. Sequence analysis revealed that the PCR-product was obtained from the corresponding HPV plasmid and matched the published sequence. Primer set SGP3/GP6 was used to confirm proper isolation of the HPV plasmids.

Table 3. HPV DNA detection by type-specific primers and general primer sets

To evaluate the efficacy of the novel primers SGP1 and SGP2 in biological samples, 92 formalin-fixed, paraffin-embedded cervical cancer biopsies were tested. A total of 61 out of the 92 biopsies were positive by type-specific PCR. Of these 61 biopsies, 54 contained HPV type 16 and 7 contained HPV type 18. The remaining 31 biopsies were assayed by HPV 31 and HPV 33 type-specific primers and remained negative. These 31 samples, negative by

type-specific PCR, were also analyzed by two general primer sets described previously. By using the MY11/MY09 and GP5/GP6 primersets only 1/31 and 3/31 biopsies were found positive, respectively. All 92 biopsies were found positive by the newly developed SGP1/SGP2 primerset.

Table 4. HPV L1 primers for the A, B and C regions

Selection of preferred primers specifically hybridizing to the A, B or C regions.

Table 5. PCR amplification with primers in the B and in the C region

The specificity of the primers listed in table 4 for the regions B and C was tested on plasmids containig polynucleic acids of HPV types 6, 11, 16, 18, 31, 33, 45, 35, 39, 58, 57 and 59. PCR was performed by all 20 possible primer combinations for the regions B and C. The results are indicated as follows:± = poor amplification; + = good; ++ = very good; blank = no amplification.

Table 6. HPV genotyping of 77 isolates by type-specific PCR and sequence analysis of the SGP1/SGP2 amplimer

77 HPV isolates positive with specific primers for type 16 or 18, were studied for sequence variability in the SGP1/SGP2 amplimer. Samples identified as type 16 by type-specific PCR were all identically typed by sequence analysis of the SGP1/SGP2 amplimer. There was no intratypic sequence variation in the small SGP1/SGP2 amplimer. Identical results were obtained for HPV 18.

Table 7. Type-specific HPV probes

Selection of preferred probes specifically hybridizing to the 22 bp region between regions B and C. "+" indicates that the probe is a sense probe; "-" refers to an antisense probe. The underlined G or C residues represent non-specific nucleotides that were added to facilitate

tailing of the probes.

Table 8. HPV primers for the synthesis of biotinylated PCR products

SGP1-bio and SGP2-bio are the biotinylated versions of SGP1 and SGP2, shown in table 1. MY09-bio is the biotinylated version of MY09, the sequence of which was disclosed in Manos et al.(1989).

Table 9. Probes for general HPV detection

Selection of preferred probes that enable detection of more than one HPV type. The types detected by each probe are listed next to the probe.

Table 10. Probes for general HPV detection

Selection of preferred probes that enable detection of more than one HPV type.

Table 11. PCR primers

Selection of preferred primers specifically hybridizing to the B or C regions.

Table 12. HPV type-specific probes

Selection of preffered probes specifically hybridizing to the region between position 6582-6646 (numbers according to HPV 16, GenBank locus name PPH16, accession number K02718). "+" indicates that the probe is a sense probe; "-" refers to an antisense probe. The underlined residues represent non HPV type-specific nucleotides.

TABLES

Table 1. HPV L1 primers in the A,B and C regions

Name	polarity	5'-sequence-3'	SEQ ID NO/ reference
		A region	
HPV16	+	TATTCAATAAACCTTATTGG	1
SGP3	+	-D--T-----R--W------	2
SGP3A	+	----T--------A------	3
SGP3B	+	----T-----G--A------	4
		B region	
MY16s	+	GCACAGGGCCACAATAATGG	5
MY11	+	--M-----W--T--Y-----	Manos et al., 1989
SGP1	+	--M-----H--T--Y-----	6
		C region	
SGP16as	-	GTATCAACAACAGTAACAAA	7
SGP2A	-	-----T--C----------	8
SGP2	-	-----H--H----------	9

D=G, A or T; R=A or G; W= A or T; M=A or C; Y=C or T; H=A, C or T.

Table 2. HPV DNA detection by the novel general primers SGP1/SGP2

HPV plasmid	SGP1/SGP2	SGP3/GP6[a]	reference[b]
3	+	+	Ostrow
4	+	-	de Villiers
5	+	+	Ostrow
5/48	+	-	de Villiers
6	+	n.d.	de Villiers
7/4	+	+	de Villiers
7/5	+	+	de Villiers
8	+	-	de Villiers
11	+	+	de Villiers
13	+	+	de Villiers
16	+	+	de Villiers
18	+	+	de Villiers
26	+	+	Ostrow
27	+	+	Ostrow
30	+	+	Orth
31	+	+	Lörinz
33	+	n.d.	Orth
35s	+	+	Lörincz
35l	+	+	Lörincz
37	+	+	de Villiers
39	+	n.d.	Orth
43s	+	+	Lörincz
43l	+	+	Lörincz
45	+	+	de Villiers
51	+	+	de Villiers

52	+	n.d.	Orth
53	+	+	de Villiers
56	+	+	Lörincz
57	+	+	de Villiers
58	+	+	Matsukura
59	+	+	Matsukura
62.2	+	+	Matsukura
64	+	+	Matsukura
65	+	+	de Villiers
67	+	+	Matsukura

[a] General primer GP6 (van den Brule et al.,1990)

[b] The HPV plasmids were kindly provided by the Dr's: Lörincz, de Villiers, Matsukura, Ostrow, ter Schegget and Orth.

Table 3. HPV DNA detection by type-specific primers and general primer sets

HPV primer set	number	HPV pos.	HPV neg.	amplimer
16	92	54	38	96 bp
18	92	7	85	115 bp
31	31[a]	0	31	110 bp
33	31[a]	0	31	114 bp
MY11/MY09	31[b]	1	30	±450 bp
GP5/GP6	31[b]	3	28	±142 bp
SGP1/SGP2	92	92	0	62 bp

a: Samples negative by type-specific primers for HPV 16 and 18

b: Samples negative by type-specific primers for HPV 16, 18, 31 and 33

Table 4. HPV L1 primers for the A, B and C regions

Name	5'-sequence-3'	SEQ ID NO
Forward primers region A		
SGP3A	TATTTAATAAACCATATTGG	3
SGP3B	TATTTAATAAGCCATATTGG	4
SGP3C	TATTTAATAAGCCTTATTGG	10
SGP3D	TATTCAATAAACCTTATTGG	11
SGP3E	TATTTAATAAACCTTACTGG	12
SGP3F	TATTTAATAAICCITATTGG	13
SGP3G	TATTTAATAAICCITACTGG	14
Forward primers region B		
SGP1A	GCICAGGGICACAATAATGG	15
SGP1B	GCICAGGGICATAACAATGG	16
SGP1C	GCICAGGGICATAATAATGG	17
SGP1D	GCICAAGGICATAATAATGG	18
Reverse primers region C		
SGP2B-bio	bio-GTIGTATCIACAACAGTAACAAA	19
SGP2C-bio	bio-GTIGTATCTACCACAGTAACAAA	20
SGP2D-bio	bio-GTIGTATCIACTACAGTAACAAA	21
SGP2E-bio	bio-GTIGTATCIACGACAGTIACAAA	22
SGP2F-bio	bio-GTIGTATCIACAACAGTIAIAAA	23

I stands for inosine

"bio-" indicates that the primer is biotinylated

Primerset	SGP1C	SGP1C	SGP1C	SGP1C	SGP1D	SGP1D	SGP1D	SGP1D	SGP1D	SGP1tot	MY11Q	SGP1AB
HPV	SGP2C-bio	SGP2D-bio	SGP2E-bio	SGP2F-bio	SGP2B-bio	SGP2C-bio	SGP2D-bio	SGP2E-bio	SGP2F-bio	SGP2tot-bio	SGP2-bio	SGP2BD-bio
6	++	++		±	+		++	±		++	++	++
11	++	++	++	+	++	±	++	+		++	±	++
16		++	++	±	±		+			++	++	++
18	++	++	++	+	++	+	++	++		++	++	++
31	++	++	++	+	++	+	++	+		++	++	++
33	++	++	++	+	++	++	++	++	+	++	++	++
45	±	+	±		+		±			++	++	++
35	±	++	++		++	++	++	++	+	++	±	++
39		++	+		++		++	++		++	±	++
58	±	+	+	±	++	++	++	+		++	++	++
57		+	++	+	+		+	++		++	+	++
59		+	++	±	+		+	±		++	++	++

Primerset	SGP1A	SGP1A	SGP1A	SGP1A	SGP1A	SGP1B	SGP1B	SGP1B	SGP1B	SGP1B	SGP1C
HPV	SGP2B-bio	SGP2C-bio	SGP2D-bio	SGP2E-bio	SGP2F-bio	SGP2B-bio	SGP2C-bio	SGP2D-bio	SGP2E-bio	SGP2F-bio	SGP2B-bio
6	+		+	+		++	++	++	++	+	++
11	++		++	+		++	++	++	++	+	++
16	++		++	++	+	++		+	+		++
18	++	+	++	++	±	++	++	++	++	+	++
31	++	++	++	++	+	++	+	++	++		++
33	++	+	++	++		++	+	++	++		++
45						++		++			+
35	+		++	±		±		++	+		++
39			+		+	±		+	+		+
58				±		++	+	++	+		+
57			+			++		+	++		+
59	±		+	±		+	+	++	++	±	+

previous page: Table 5. PCR amplification with primers in the B and in the C region

Table 6. HPV genotyping of 77 isolates by type-specific PCR and sequence analysis of the SGP1/SGP2 amplimer.

HPV-type	type-specific PCR	SGP1/SGP2
16	70	70
18	7	7

Table 7. Type-specific HPV probes

Name	5'-sequence-3'	polarity	SEQ ID NO
HPV6 Pr1	TTGGGGTAATCAACTGTGG	+	24
HPV6 Pr2	GTTGGGGTAATCAACTGTGG	+	25
HPV6 Pr3	TTGGGGTAATCAACTGTTG	+	26
HPV6 Pr4	GTTGGGGTAATCAACTGTTG	+	27
HPV6 Pr5	TTGGGGTAATCAACTGTTT	+	28
HPV11 Pr1	TGCTGGGGAAACCACTG	+	29
HPV11 Pr2	TGCTGGGGAAACCACTTAGG	+	30
HPV11 Pr3	TTGTTGGGGAAACCACTG	+	31
HPV11 Pr4	TTGCTGGGGAAACCACTTAGG	+	32
HPV11 Pr5	TGCTGGGGAAACCACTTGGG	+	33
HPV16 Pr1	TTGGGGTAACCAACTATGG	+	34
HPV16 Pr2	GTTGGGGTAACCAACTATGG	+	35
HPV16 Pr3	TTGGGGTAACCAACTATTG	+	36
HPV16 Pr4	GTTGGGGTAACCAACTATTG	+	37
HPV16 Pr5	TTGGGGTAACCAACTATTT	+	38
HPV18 Pr1	GTGTTTGCTGGCATAAT	+	39
HPV18 Pr2	GGTGTTTGCTGGCATAAG	+	40
HPV18 Pr3	GTGTTTGCTGGCATAATC	+	41
HPV18 Pr4	TGGTGTTTGCTGGCATAAG	+	42
HPV18 Pr5	GGTGTTTGCTGGCATAAT	+	43
HPV31 Pr1	TTGGGGCAATCAGTTATGG	+	44
HPV31 Pr2	GTTGGGGCAATCAGTTATGG	+	45
HPV31 Pr3	TTGGGGCAATCAGTTATTG	+	46
HPV31 Pr4	GTTGGGGCAATCAGTTATTG	+	47
HPV31 Pr5	GTTGGGGCAATCAGTTATTT	+	48
HPV31 Pr21	GGGCAATCAGTTATTG	+	49
HPV31 Pr22	AATAACTGATTGCCC	-	50
HPV31 Pr23	GGCAATCAGTTATTTCC	+	51
HPV31 Pr24	AAATAACTGATTGCC	-	52

HPV31 Pr25	GCAATCAGTTATTTGG	+	53
HPV31 Pr26	CAAATAACTGATTGC	-	54
HPV31 Pr31	GGCAATCAGTTATTTGG	+	55
HPV31 Pr32	GCAATCAGTTATTTGTG	+	56
HPV33 Pr1	TTGGGGCAATCAGGTATGG	+	57
HPV33 Pr2	GTTGGGGCAATCAGGTATGG	+	58
HPV33 Pr3	TTGGGGCAATCAGGTATTG	+	59
HPV33 Pr4	GTTGGGGCAATCAGGTATTG	+	60
HPV33 Pr5	GTTGGGGCAATCAGGTATTT	+	61
HPV33 Pr21	GGGCAATCAGGTATTG	+	62
HPV33 Pr22	AATACCTGATTGCCC	-	63
HPV33 Pr23	GGCAATCAGGTATTTCC	+	64
HPV33 Pr24	AAATACCTGATTGCC	-	65
HPV33 Pr25	GCAATCAGGTATTTGG	+	66
HPV33 Pr26	CAAATACCTGATTGC	-	67
HPV40 Pr1	CATATGTTTTGGCAATC	+	68
HPV45 Pr1 = SGPP68	GTATTTGTTGGCATAAT	+	69
HPV45 Pr2	GGTATTTGTTGGCATAAG	+	70
HPV45 Pr3	GTATTTGTTGGCATAATC	+	71
HPV45 Pr4	TGGTATTTGTTGGCATAAG	+	72
HPV45 Pr5	GGTATTTGTTGGCATAAT	+	73
HPV45 Pr11	TGGCATAATCAGTTGGG	+	74
HPV45 Pr12	GGCATAATCAGTTGTG	+	75
HPV45 Pr13	GCATAATCAGTTGTTT	+	76
HPV52 Pr1	GCAATCAGTTGTTTGC	+	77
HPV52 Pr2	CAATCAGTTGTTTGTC	+	78
HPV52 Pr3	ATGGCATATGTTGGG	+	79
HPV52 Pr4	TGGCATATGTTGGGGG	+	80
HPV52 Pr5	GGCATATGTTGGGGC	+	81
HPV52 Pr6	GCATATGTTGGGGCA	+	82
HPV56 Pr1	GGGGTAATCAATTATC	+	83
HPV56 Pr2	GGGGTAATCAATTATTC	+	84
HPV56 Pr3	GGGGTAATCAATTATTT	+	85
HPV56 Pr11	TGGGGTAATCAATTATTT	+	86

HPV56 Pr12	GGGGTAATCAATTATTTGG	+	87
HPV58 Pr1	CATTTGCTGGGGCAAG	+	88
HPV58 Pr2	ATTTGCTGGGGCAAT	+	89
HPV58 Pr3	TTTGCTGGGGCAATC	+	90
HPV58 Pr4	TTGCTGGGGCAATCA	+	91
SGPP35	GTTGGAGTAACCAATTG	+	92
SGPP39	GTATATGTTGGCATAAT	+	93
SGPP51 = HPV51 Pr1	GCATTTGCTGGAACAAT	+	94
SGPP54	GGGGCAATCAGGTGTTT	+	95
SGPP59	GGTATATGTTGGCACAA	+	96
SGPP66	GCATATGCTGGGGTA	+	97
SGPP68 = HPV45 Pr1	GTATTTGTTGGCATAAT	+	69
SGPP70 = HPV70 Pr11	CATTTGTTGGCATAACC	+	99
SGPP13	TGGGGCAATCACTTG	+	100
SGPP34	GCATTTGCTGGCATA	+	101
SGPP42	TGGGGAAATCAGCTATT	+	102
SGPP43	GGCATTTGTTTTGGGAA	+	103
SGPP44	TTGGGGAAATCAGTTATT	+	104
SGPP53	GCATCTGTTGGAACAA	+	105
SGPP55	GTTGGGGGAATCAGT	+	106
SGPP69	GTTGGGGCAACCAATTG	+	107
SGPP61	TGGTTTAATGAATTGTTT	+	108
SGPP62	GGTTTAATGAACTGTTT	+	109
SGPP64	AATGGAATTTGTTGGCA	+	110
SGPP67	GTATATGCTGGGGTAAT	+	111
SGPP74 = HPV74 Pr13	ATTTGTTGGGGTAATCA	+	112
MM4 = HPVM4Pr11	TGCTGGAATAATCAGCT	+	113
MM7	TGGTTTAATGAGTTATTT	+	114
MM8	ATATGCTGGTTTAATCA	+	115

Table 8. HPV primers for synthesis of biotinylated PCR products.

Name	polarity	5'-sequence-3'	SEQ ID NO/ reference
SGP1-bio	+	bio-GCMCAGGGHCATAAYAATGG	6
SGP2-bio	-	bio-GTATCHACHACAGTAACAAA	9
MY09-bio	-	bio-CGTCCMARRGGAWACTGATC	Manos et al., 1989

M=A or C; H=A, C or T; Y=C or T; R=A or G; W=A or T

Table 9. Probes for general HPV detection

Name	5'-sequence-3'[1]	position[2]	HPV types recognized	SEQ ID NO
HPVuni1	AATAATGGCATITGTTGG	6594-6611	16,30,52,53, 70,MM7,72,43	116
HPVuni2	AATAATGGTATITGTTGG	6594-6611	31,33,26,35, 13,42,44,55, 62,73	117
HPVuni3	AACAATGGTATITGTTGG	6594-6611	45,6,59,68, 54,61,39	118
HPVuni4	AACAATGGTATITGCTGG	6594-6611	11,67,MM8	119
HPVuni5	AACAATGGTGTTTGCTGG	6594-6611	18	120
HPVuni6	AATAATGGCATITGCTGG	6594-6611	51,56,66,MM4	121
HPVuni7	AACAATGGCATITGCTGG	6594-6611	34,57,58	122
HPVuni1A	CAIAATAATGGCATITGTTGGC	6591-6612	16,30,52,53, 70,MM7,72,43	220
HPVuni1B	CAIAACAATGGCATITGTTGGC	6591-6612	16,30,40,52,5 3,69,70,MM7 72,43	221
HPVuni1C	CACAATAATGGCATTTGTTGGGG	6591-6613	16,30,52,53, 70,MM7,72,43	222
HPVuni2A	CAIAATAATGGTATITGTTGGG	6591-6612	31,33,26,35, 13,42,44,55, 62,73	223
HPVuni3A	CAIAACAATGGTATITGTTGGC	6591-6612	45,6,59,68, 54,61,39	224

[1] I = inosine

[2] Sequence positions according to HPV genotype 16 sequence PPH16, Genbank accession number K02718

HPV type 64 is theoretically not recognised.

Table 10. Probes for general HPV detection

Name	5'-sequence-3'	polarity	SEQ ID NO
HPVuni2L2	CAIAATAATGGTATITGTTGG	+	123
HPVuni2L3	AIAATAATGGTATITGTTGG	+	124
HPVuni2L4	CAIAATAATGGTATTTGTTGG	+	125
HPVuni2L5	AIAATAATGGTATTTGTTGG	+	126
HPVuni2L6	CACAATAATGGTATTTGTTGG	+	127
HPVuni2L7	ACAATAATGGTATTTGTTGG	+	128
HPVuni4L1	CAIAACAATGGTATITGTTGG	+	129
HPVuni4L2	AIAACAATGGTATITGTTGG	+	130
HPVuni4L3	CAIAACAATGGTATTTGTTGG	+	131
HPVuni4L4	AIAACAATGGTATTTGTTGG	+	132
HPVuni4L5	CATAACAATGGTATTTGTTGG	+	133
HPVuni4L6	ATAACAATGGTATTTGTTGG	+	134
HPV G1	AATGGCATTTGTTGGGGTAACCAACTATTT	+	225
HPV G1A1	TTGTTGGGGTAACCAACTATG	+	226
HPV G1A2	ATTTGTTGGGGTAACCAACTATTG	+	227
HPV G1A3	GCATTTGTTGGGGTAACCAACTA	+	228
HPV G1A4	TGGCATTTGTTGGGGTAACCAACTA	+	229
HPV G2	AATGGTATTTGTTGGGGCAATCAGTTATTT	+	230
HPV G3	AATGGTATTTGTTGGCATAATCAGTTGTTT	+	231
HPV G4	AATGGTATTTGTTGGTTTAATGAATTGTTT	+	232
HPV G5	AATGGCATTTGCTGGAACAATCAGCTTTTT	+	233
HPV G6	AATGGTATATGTTGGGGCAATCACTTGTTT	+	234
HPV R1	AATGGCATTTGTTGGGGC	+	235
HPV R10	AATGGCATATGCTGGAATAATC	+	236
HPV R11	AATGGTATATGTTGGGGCAATC	+	237
HPV R2	AATGGTATTTGTTGGGGC	+	238

HPV R3	AATGGAATTTGTTGGCATAATC	+	239
HPV R4	GGTATCTGCTGGCATAAT	+	240
HPV R5	AATGGCATTTGTTGGTTTAATG	+	241
HPV R6	AATGGTATTTGTTGGTTTAATG	+	242
HPV R7	AATGGCATCTGTTGGTTTAATG	+	243
HPV R8	TGTTGGTTTAATGAGCTGTG	+	244
HPV R9	TGCTGGTTTAATCAATTGTTG	+	245

Underlined sequences are not complementary to HPV.

Table 11. PCR primers

Primer designation	5'-sequence-3'[1]	position[2]	SEQ ID NO
SGP1A	GCICAGGGICACAATAATGG	6582-6601	15
SGP1B	GCICAGGGICATAACAATGG	6582-6601	16
SGP1C	GCICAGGGICATAATAATGG	6582-6601	17
SGP1D	GCICAAGGICATAATAATGG	6582-6601	18
SGP2B-bio	GTIGTATCIACAACAGTAACAAA	6624-6646	19
SGP2D-bio	GTIGTATCIACTACAGTAACAAA	6624-6646	21
SGP2H-bio	GTIGTATCIACAACTGTAACAAA	6624-6646	98
SGP2I-bio	GTIGTATCCACAACAGTTACAAA	6624-6646	154
SGP2J-bio	GTGGTATCCACAACIGTGACAAA	6624-6646	155
SGP2K-bio	GTAGTITCCACAACAGTAAGAAA	6624-6646	156
SGP2L-bio	GTAGTATCAACCACAGTTAAAAA	6624-6646	157
SGP2M-bio	GTIGTATCTACAACIGTTAAAAA	6624-6646	158
SGP2N-bio	GTAGTATCTACACAAGTAACAAA	6624-6646	159
SGP2P-bio	GTAGTATCAACACAGGTAATAAA	6624-6646	160

[1] I = inosine

[2] Sequence positions according to HPV genotype 16 sequence PPH16, Genbank accession number K02718.

Table 12. HPV type-specific probes

HPV PROBE	5'-sequence-3'	polarity	SEQ ID NO
HPV18b Pr1	GGTATCTGCTGGCATAAG	+	161
HPV18b Pr2	TGGTATCTGCTGGCATA	+	162
HPV31 Vs40-1	TATTTGTTGGGGCAATC	+	163
HPV31 Vs40-2	ATTTGTTGGGGCAATC	+	164
HPV31 Vs40-3	TATTTGTTGGGGCAAT	+	165
HPV34 Pr1	GGCATTTGCTGGCATA	+	166
HPV35 Pr1	GTTGGAGTAACCAATTGGG	+	167
HPV35 Pr2	TGTTGGAGTAACCAATTCC	+	168
HPV35 Pr3	TTGTTGGAGTAACCAATG	+	169
HPV39 Pr1	GGTATATGTTGGCATAAT	+	170
HPV42 Pr1	GGGGAAATCAGCTATTG	+	171
HPV42 Pr2	GGGAAATCAGCTATTT	+	172
HPV43 Pr1	GGCATTTGTTTTGGGAAG	+	173
HPV43 Pr2	GCATTTGTTTTGGGAAT	+	174
HPV43 Pr3	CATTTGTTTTGGGAATC	+	175
HPV44 Pr1	GGGGAAATCAGTTATTG	+	176
HPV44 Pr2	GGGGAAATCAGTTATTT	+	177
HPV44 Pr3	GGGAAATCAGTTATTT	+	178
HPV44 Pr4	TGGGGAAATCAGTTATG	+	179
HPV45 Pr5	GGTATTTGTTGGCATAAT	+	73
HPV51 Pr1 = SGPP51	GCATTTGCTGGAACAAT	+	94
HPV51 Pr2	CATTTGCTGGAACAATC	+	180
HPV53 Pr1	GGCATCTGTTGGAACAA	+	181
HPV54 Pr1	GGCAATCAGGTGTTTC	+	182
HPV54 Pr11	GGGCAATCAGGTGTTTC	+	183
HPV54 Pr11as	AAACACCTGATTGCCC	-	184
HPV54 Pr12	GGCAATCAGGTGTTTTG	+	185
HPV55 Pr1	GGGGGAATCAGTTATTG	+	186
HPV55 Pr11	GGGGGAATCAGTTATG	+	187

HPV55 Pr12	TGGGGGAATCAGTTATG	+	188
HPV55 Pr13	TGGGGGAATCAGTTAG	+	189
HPV56 Vs74-1	CATTTGCTGGGGTAAT	+	190
HPV59 Pr1	TGGTATATGTTGGCACAA	+	191
HPV59 Pr11	GGTATATGTTGGCACAAT	+	192
HPV59 Pr12	GTATATGTTGGCACAATC	+	193
HPV59 Pr13	TATATGTTGGCACAATC	+	194
HPV66 Pr1	GGCATATGCTGGGGTA	+	195
HPV67 Pr1	GGTATATGCTGGGGTAAT	+	196
HPV67 Pr11	GGTATATGCTGGGGTA	+	197
HPV67 Pr12	TGGTATATGCTGGGGT	+	198
HPV67 Pr13	ATGGTATATGCTGGGGG	+	199
HPV67 Pr21	GGTATATGCTGGGGT	+	200
HPV67 Pr22	TGGTATATGCTGGGGG	+	201
HPV67 Pr23	AATGGTATATGCTGGG	+	202
HPV68 Pr1	TGGTATTTGTTGGCATA	+	203
HPV68 Pr2	ATGGTATTTGTTGGCATA	+	204
HPV68 Pr3	ATGGTATTTGTTGGCAT	+	205
HPV68 Vs45-1	TTGGCATAATCAATTATTT	+	206
HPV68 Vs45-2	TTGGCATAATCAATTATTTCG	+	207
HPV70 Pr1	GCATTTGTTGGCATAACC	+	208
HPV70 Pr11 = SGPP70	CATTTGTTGGCATAACC	+	99
HPV70 Pr12	GCATTTGTTGGCATAAC	+	209
HPV70 Pr13	CATTTGTTGGCATAAC	+	210
HPV74 Pr1	TATTTGTTGGGGTAAT	+	211
HPV74 Pr11	ATTTGTTGGGGTAATC	+	212
HPV74 Pr12	TTTGTTGGGGTAATCA	+	213
HPV74 Pr13 = SGPP74	ATTTGTTGGGGTAATCA	+	112
HPV74 Pr2	GTATTTGTTGGGGTAAT	+	214
HPV74 Pr3	TATTTGTTGGGGTAATC	+	215
HPVM4 Pr1	TTGCTGGAATAATCAGCT	+	216
HPVM4 Pr11 = MM4	TGCTGGAATAATCAGCT	+	113

HPVM4 Pr12	TGCTGGAATAATCAGC	+	217
HPVM4 Pr21	TGCTGGAATAATCAGCTG	+	218
HPVM4 Pr22	TGCTGGAATAATCAGCG	+	219

Underlined sequences are not complementary to HPV

EXAMPLES

The following examples only serve to illustrate the present invention. These examples are in no way intended to limit the scope of the present invention.

Example 1: Development of novel general HPV PCR primers.

Introduction

The aim of the present example was to deduce PCR primers that allow general PCR amplification of sequences from multiple HPV types.

Materials and methods

Design of primers

HPV sequences were obtained from the GenBank database.

Alignment of all available L1 sequences revealed that there are several regions that show a high degree of conservation among the different HPV genotypes. These regions are indicated in figure 1 and are designated A,B and C, respectively.

In order to obtain universal amplification of all HPV sequences, several primers were selected in these three regions. The locations and sequences of the different primers are represented in figure 2 and table 1, respectively. Primer combinations from the A (SGP3) and C (SGP2) region and those from the B (SGP1) and C (SGP2) region will yield an expected amplimer of 91 basepairs (bp) or 62 bp, respectively. Type-specific primers for HPV types 16, 18, 31 and 33 were described in Baay et al.(1996). The MY11-MYO9 primer set was described in Manos et al. (1989). The GP5/GP6 primer set was described in van den Brule et al. (1990).

DNA isolation

DNA was isolated from the 92 formalin fixed and paraffin-embedded cervical cancer biopsies by a modified version of the method described by Claas et al (1989). A 10 µm section was collected in a 1.5 ml tube and deparaffinized by 500 µl Xylol. After gently shaking for 2 minutes and centrifugation for 5 minutes the pellet was again treated with 500

µl Xylol. The pellet was washed twice with 500 µl alcohol 96% and once with 500 µl acetone. Subsequently, the pellet was air-dried and treated with a 200 µl proteinase K solution (1 mg/ml) overnight at 37°C.

PCR

The PCR was performed essentially as described by Saiki (1988). Briefly, the final volume of 100 µl contained 10 µl of the isolated DNA, 10mM Tris-HCl pH 9.0, 50 mM KCl, 2.5 mM $MgCl_2$, 0.1% Triton X-100, 0.01% gelatin, 200 µM of each deoxynucleoside triphosphate, 50 pmol of forward and reverse primer, and 0.25U of SuperTaq (Sphaero Q, Cambridge, United Kingdom). For the MY11/MY09 primerset (Manos et al., 1989) 0.5U SuperTaq was used. PCR conditions were a preheating step for 1 min 94°C followed by 40 cycles of 1 min 94°C, 1 min 52°C and 1 min 72°C. For the primerset SGP3/SGP2 the 40 cycles of amplification consisted of 1 min 94°C, 1 min 40°C and 1 min 72°C. For the primerset GP5/GP6 (van den Brule et al., 1990) the 40 cycles of amplification consisted of and 1 min 94°C, 2 min 40°C and 1.5 min 72°C. As a control for succesful DNA isolation a PCR was performed using ß-globin primers described by Saiki (1986).

Southern blot analysis

The Southern blot hybridization experiments were performed according to standard procedures (Sambrook et al., 1989). Briefly, 20 µl of the PCR-product was electrophoresed on a 2% agarose gel. Amplimers produced by the primer sets SGP1/SGP2 and SGP3/SGP2 were applied on a 3% agarose gel. Subsequently, amplimers were transferred to a nylon membrane (Hybond N+, Amersham, Little Chalfont, United Kingdom) by vacuum blotting in the presence of 0.4N NaOH. The Southern blots were hybridized with a ^{32}P 5'-end labeled probe(s) for 16 hours at 42°C in a solution containing 5x SSC (1x SSC: 15 mM Na-citrate and 150 mM NaCl, pH 7.0), 5x Denhardt's (1x Denhardt: 0.02% bovine serum albumin, 0.02% polyvinyl pyrolidone and 0.02% ficoll), 0.5% SDS, 75 mM EDTA and 0.1mg/ml herring sperm DNA. Subsequently, the blots were washed twice in 2x SSC/0.1% SDS at 42°C for 15 minutes. Autoradiography was performed for 3.5 hours using the Kodak X-Omat AR film.

Samples that were negative by type-specific primers were also analyzed by the L1

directed general primer sets MY11/MY09 and GP5/GP6.

Sequence analysis

PCR products were analyzed by direct sequencing, using a cycle-sequencing kit (Perkin Elmer). Sequences were analyzed by the PC-Gene software (Intelligenetics, USA)

Results

In order to develop a general set of PCR primers that would allow universal amplification of HPV sequences, we aimed at the L1 region. Primers SGP1 and SGP2 were tested on a number of plasmids, containing partial or complete genomic sequences from various HPV types. The results are summarized in table 2. An amplimer was obtained for all HPV plasmids by the SGP1/SGP2 primer set, although the amount of PCR-product was different. Sequence analysis revealed that the PCR-product was obtained from the corresponding HPV plasmid and matched the published sequence. Primer set SGP3/GP6 was used to confirm proper isolation of the HPV plasmids.

To evaluate the efficacy of the novel primers SGP1 and SGP2 in biological samples, 92 formalin-fixed, paraffin-embedded cervical cancer biopsies were tested.

DNA isolated from these biopsies was subjected to different PCR assays: ß-globin primers PCO3 and PCO4 (Saiki et al., 1988), SGP1/SGP2, and type-specific PCR for HPV types 16, 18, 31, and 33. The results are summarized in table 3.

1. All biopsies contained amplifiable DNA as determined with PCR directed to the ß-globin gene.

2. A total of 61 (66%) of the 92 biopsies were positive by type-specific PCR. Of these 61 biopsies, 54 contained HPV type 16 and 7 contained HPV type 18. Subsequently, the remaining 31 biopsies were assayed by HPV 31 and HPV 33 type-specific primers and remained negative.

3. The 31 samples, negative by type-specific PCR were also analyzed by two general primer sets described previously (Manos et al., 1989; van den Brule et al., 1990). By using the MY11/MY09 and GP5/GP6 primersets only 1/31 and 3/31 biopsies were found positive, respectively.

4. All 92 biopsies were found positive by the newly developed SGP1/SGP2 primerset.

Discussion

In general, amplification of a small genomic fragment is likely to increase the sensitivity of the PCR. This is of particular importance when using biological samples that contain a very low copy number of HPV. Furthermore, cervical biopsies that have been formalin-fixed and paraffin-embedded are a poor source of amplifiable DNA.

In this high-risk group for HPV, the novel primer combination SGP1/SGP2 was more sensitive than the type-specific PCR and the general PCRs that were also directed to the L1 region of HPV.

In conclusion the newly developed primer sets are highly sensitive for detection of HPV DNA.

Example 2: Optimization of PCR primers from the A, B and C region.

Introduction

Example 1 describes the selection of semi-conserved regions in the L1 gene of the HPV genome, that permitted the development of a general PCR system. Degenerated primers were used for universal amplification of HPV sequences from different genotypes.

The present example describes the optimization of the primers aimed at these regions. Instead of degenerated primers, this study aimed at the development of several distinct and defined forward and reverse primers.

Materials and Methods

Alignments of L1 sequences were used to deduce PCR primers from the three regions A, B and C (figure 1). Primers were tested by PCR in different combinations on plasmids, containing partial or complete genomic inserts from the genital HPV types 6, 11, 16, 18, 31, 33, 35, 39, 43, 45, 51, 52, 53, 56, 57, 58, 59, 62, 64 and 67 as listed in table 2.

HPV DNA amplification was performed according to the following protocol. The final PCR volume of 100 µl contained 10 µl of HPV plasmid DNA, 75 mM Tris-HCl pH 9.0, 20 mM $(NH_4)_2SO_4$, 2,5 mM $MgCL_2$, 0.1% (w/v) Tween 20, 200 µM of each deoxynucleoside triphosphate, 100 pmol of forward and reverse primer, and 3U of Taq-DNA polymerase

(Pharmacia, Uppsala, Sweden). After a preheating step for 1 min 94°C amplification was performed by 1 min 94°C, 1 min 52°C and 1 min 72°C for 40 cycles. Subsequently, PCR-products were analyzed on a 3% agarose gel.

Results

Based on the alignments of the L1 sequences as shown in figure 1, primers were selected, as shown in table 4. The specificity of the primers in the regions B and C was tested on the plasmids HPV 6, 11, 16, 18, 31, 33, 45, 35, 39, 58, 57 and 59. PCR was performed by all 20 possible primer combinations for the regions B and C and results are summarized in table 5. Poor results were only obtained when using the primer SGP2F-bio that contains an inosine residu at four positions. Although some primer sets had mismatches with the target HPV sequences, amplimers were synthesized for all tested HPV plasmids. From the tested nine primers in the regions B and C, four of them (SGP1A, SGP1B, SGP2B-bio and SGP2D-bio) could be used for efficient HPV amplification. PCR performance of the primer set containing the four primers SGP1A, SGP1B, SGP2B and SGP2D revealed amplification from all tested HPV plasmids: 6, 11, 16, 18, 31, 33, 45, 35, 39, 58, 57 and 59.

Sequence analysis of the amplimers revealed the expected sequence for each plasmid. This result indicates that the four primers are able to detect the various HPV types. The mismatches with especially type 57 and 59 apparently did not hamper amplification.

Discussion

Despite the presence of mismatches between primer and target sequence, successful amplification by PCR may occur if there are no mismatches at the 3' end of the primer. The PCR and sequence data obtained in this study indicate that the primers SGP1A, SGP1B, SGP2B-bio and SGP2D-bio are able to detect efficiently the various HPV genotypes. Therefore, these four primers can be used for universal amplification of HPV.

Example 3: Identification of different HPV types by analysis of a small PCR fragment derived from the L1 region.

Introduction

Identification of the different HPV genotypes may have great clinical and epidemiological importance. Current classification methods are for instance based on either type-specific PCR or sequence analysis of larger DNA fragments. Therefore, there is a clear need for a simple, rapid and reliable genotyping assay for the different HPV genotypes.

This assay should preferably be combined with the detection of HPV DNA, aiming at the same genomic region. Therefore, we aimed at the development of a screening assay to detect the presence of HPV DNA in clinical samples, and (in case of a positive screening result) the subsequent use of the same amplimer in a genotyping assay.

The theoretical requirements for such an assay would be as follows:

1. The amplimer should be small, to allow highly sensitive detection and to permit amplification from formalin-fixed, paraffin-embedded materials. The development of such a PCR assay has been described in examples 1 and 2.

2. The amplified fragment should contain sufficient sequence variation to permit specific detection of the different genotypes.

The present study describes: (i) the relationship between sequences from the various HPV types by phylogenetic analyses of the regions MY11/MY09, the sequence between region A and C (51 bp) and between B and C (22 bp); (ii) the analysis of the small amplimer of 62 bp generated by primers from the region B and C; (iii) The development of HPV type-specific probes from this region.

Materials and methods

1. Sequences from the different HPV genotypes were obtained from the GenBank database.
2. Phylogenetic analyses were performed with the Phylip 3.5c software (Felsenstein 1995).
3. Type-specific HPV PCR and general HPV amplification by SGP1/SGP2 were performed according to the protocol as described in examples 1 and 2.
4. Sequence analysis of the PCR-products was performed by manual sequencing, using the cycle-sequencing kit (Perkin Elmer). Sequences were analyzed by the PC-Gene software

(Intelligenetics, USA)

Results

Phylogenetic analyses

In order to study the relationships between the HPV-derived sequences, several phylogenetic trees were constructed.

1. Sequences between primers MY11 and MY09 were selected from all available HPV sequences. The phylogenetic tree is shown in figure 3. Sequence variation in this ±410 bp region permits discrimination between most, if not all HPV genotypes. The different groups of HPV (indicated with an A followed by a number) are indicated in the figure (Chan et al., 1995).

2. Sequences between the regions A and C and those between B and C were also subjected to phylogenetic analysis, and both trees are shown in the figure 4 and figure 5, respectively. Sequence variation enclosed by the primers in regions B and C (22bp) allows discrimination between the genital HPV types. HPV68 (a genital type) and HPV73 (an oral type) show an identical sequence in this region. However these two types can be recognized in the region flanked by primers in the regions A and C, for instance by use of probes HPV 68 (CAGGGACACAACAATG) and HPV 73 (CAGGGTCATAACAATGG).

Intratypic variation

Since the aim of this study is to determine whether the intratypic sequence variation in the small PCR product is sufficient to identify the different HPV genotypes, the intratypic variation should also be investigated.

Therefore, 77 HPV isolates positive with specific primers for type 16 or 18, were studied for sequence variability in the SGP1/SGP2 amplimer. Samples identified as type 16 by type-specific PCR were all identically typed by sequence analysis of the SGP1/SGP2 amplimer (table 6). There was no intratypic sequence variation in the small SGP1/SGP2 amplimer. Identical results were obtained for HPV 18.

Sequence analysis of the SGP1/SGP2 amplimers in the group of 31 samples negative by HPV type-specific PCR, as described in example I, revealed different HPV sequences. The obtained sequences were identical to HPV types 16 (n=9), 18 (n=4), 31 (n=2), 35 (n=1), 45

(n=5), 52 (n=2), 56 (n=3) and 58 (n=2). This indicates that PCR with SGP1/SGP2 is more sensitive than HPV type-specific PCRs. Aberrant sequences, not matching any known HPV type, were found in three cases. It was not possible to amplify these isolates by other previously described general primer sets (MY11/MY09, GP5/GP6 and CPI/CPIIg). For these samples the HPV specificity was confirmed by performing a semi-nested PCR with the primer sets SGP3/SGP2 and SGP1/SGP2.

Discussion

Phylogenetic analyses of the various HPV types revealed heterogeneity in the region between primers SGP1 and SGP2. Sequence variation was found to be sufficient for consistent discrimination between all genital HPV types. In order to investigate the reproducibility of this region for HPV genotyping, 77 samples were typed by type-specific PCR and sequence analysis of the SGP1/SGP2 amplimer. No intratypic variation was observed in the SGP1/SGP2 amplimers.

From these results and that of already reported sequences, in particular HPV type 16 variants, it might be suggested that intratypic variability in the 22bp between the SGP1 and SGP2 primers is very limited. This observation supports the use of sequence variation in the SGP1/SGP2 amplimer for HPV genotyping.

Example 4: Development of the HPV INNO-LiPA genotyping assay

Introduction

An aim of the invention was to develop a simple and reliable system for detection as well as identification of HPV genotypes. A possible format of such a system could comprise a single PCR using universal primers, that amplify a small genomic fragment with very high sensitivity. Subsequently, the same PCR product can be used to discriminate between the HPV genotypes.

For analysis of the PCR products, sequence analysis is a very accurate method, but it is not very convenient. Therefore we aimed at the development of type-specific probes, that would permit positive recognition of the different HPV genotypes.

Materials and methods

Selection of probes:

Based on the 22 bp sequences located between the regions B and C (figure 1), a number of type-specific probes were proposed. These probes are listed in table 7.

HPV plasmids and clinical isolates

The selected probes were analysed for analytical and clinical specificity. First, plasmids, containing complete genomic sequences of different HPV types, were used as target for PCR amplification with primers SGP1-bio and SGP2-bio, and with primers SGP1-bio and MY09-bio.

PCR reactions

PCR was performed using the primer sets SGP1-bio/SGP2-bio and SGP1-bio/MY09-bio. All primers contained a biotin moiety at the 5' end (table 8). The PCR conditions were similar to those described in example 1. The final volume of 100 µl contained 10 µl of plasmid DNA, 75 mM Tris-HCl pH 9.0, 20 mM $(NH_4)_2SO_4$ 2,5 mM $MgCl_2$ 0.1% (w/v) Tween 20, 200 µM of each deoxynucleoside triphosphate, 100 pmol of forward and reverse primer, and 3U of Taq-DNA polymerase (Pharmacia, Uppsala, Sweden). After a preheating step for 1 min 94°C amplification was performed by 1 min 94°C, 1 min 52°C and 1 min 72°C for 40 cycles.

Development of a Reverse Hybridization format

In order to permit analysis of multiple probes in a single hybridization step, a reverse hybridization assay was developed. This requires the selection of type-specific probes that have very similar hybridization characteristics. For this experiment probes were chosen for HPV types 6, 11, 16, 18, 31, 33 and 45.

Oligonucleotide probes were provided with a poly-(dT) tail at the 3' end. Twenty pmol primer was incubated in 25µl buffer containing 3.2 mM dTTP, 25 mM Tris-HCl (pH 7.5), 0.1 M sodium cacodylate, 1 mM $CoCl_2$, 0.1 mM dithiothreitol and 60 U terminal desoxynucleotidyl transferase for 1 h at 37°C. The reaction was stopped by adding 2.5 µl 0.5 M EDTA (pH 8.0) and diluted with 20 x SSC (Sambrook et al., 1989), until a final

concentration of 6 x SSC and 2.5 pmol oligonucleotide/µl was reached. The tailed probes were immobilized on a nitrocellulose strip as parallel lines. As a control for the conjugate, biotinylated DNA was also applied. A possible outline of the strip is shown in figure 6.

Ten µl of the PCR amplification product, containing biotin at the 5' end of each primer, was mixed with 10 µl of denaturation solution (400 mM NaOH, 10 mM EDTA) and incubated at room temperature for 10 minutes. After denaturation of the DNA, 1 ml of preheated hybridization buffer, 3 x SSC, 0.1 % SDS, (1 x SSC: 15 mM Na-citrate and 150 mM NaCl) was added. The hybridization was performed at 50°C in a shaking waterbath for 1 h. The strips were washed once with hybridization buffer at 50°C for 30 minutes. The strips were then washed by rinse solution (phosphate buffer containing NaCl, Triton and 0.5% NaN_3). Alkaline phosphatase labelled streptavidin was added in conjugate diluent (phosphate buffer containing NaCl, Triton, protein stabilizers and 0.1% NaN_3) and incubated at 37°C for 1 h. Strips were washed again three times with rinse solution and once with substrate buffer (Tris buffer containing NaCl and $MgCl_2$). Colour development was achieved by addition of BCIP and NBT in substrate buffer and incubation for 30 minutes at room temperature. Colour development was stopped by incubation in water and drying of the strips. Reverse hybridization results were interpreted visually.

Results and discussion

In order to develop a novel HPV typing assay, we selected probes from a small part of the L1 region. This approach would first require detection of HPV sequences in general by PCR using universal primers, such as SGP1/SGP2, generating a fragment of 62 bp or MY11/MY09, generating a fragment of approximately 450 bp. Subsequently, the same PCR product can be analysed using type-specific probes from this L1 region.

PCR fragments of 62 bp and 450 bp were generated by primer sets SGP1-bio/SGP2-bio and SGP1-bio/MY09-bio, respectively from different target DNA.

First, plasmids containing complete genomic sequences from the HPV types 6; 11, 16, 18, 31, 33 and 45 were subjected to PCR with primerset SGP1-bio/SGP2-bio. Subsequently, the amplimers were analysed in the reverse hybridization assay containing type-specific probes for recognition of the HPV types 6, 11, 16, 18, 31, 33 and 45. Representative results of reverse hybridization are shown in figure 7. Secondly, amplimers synthesized by the

primerset SGP1-bio/MY09-bio from HPV types 6, 16, 31, 33 and 45 were analysed in the reverse hybridization assay (figure 8).

The results show that the method has a high sensitivity and allows detection of HPV sequences at very low concentrations or from difficult clinical materials, such as formalin-fixed, paraffin-embedded biopsies. The reverse hybridization method permits positive identification of the main HPV genotypes 6, 11, 16, 18, 31, 33 and 45. This assay can easily be extended by adding probes on the strip for recognition of all other genital HPV genotypes.

Example 5: Sequencing of HPV isolates

Introduction

In this study, the sequence of HPV isolates in the region between primers SGP1 and SGP2 was analyzed.

Materials and Methods

DNA was isolated from formalin-fixed and paraffin-embedded cervical cancer biopsies and cytologically abnormal scrapes according to standard protocols. PCR was performed as described in example 1 by the use of primers SGP1 and SGP2. The obtained amplimers were analyzed by direct sequencing.

Results

Sequencing of HPV-positive samples revealed that, within the region between primers SGP1 and SGP2, 19 sequences from different patients were aberrant from previously described full-length HPV types. These previously unknown sequences are listed in Figure 1. Sequences having an identification number starting with 95, were found in cervical cancer biopsies, whereas those starting with 97 were found in cytologically abnormal scrapes.

Discussion

Any of the 19 sequences disclosed in this study may be representative for a new HPV type. Further investigation will be carried out to determine whether indeed any of these

sequences is characteristic of a new HPV type that is possibly clinically important. Probes that specifically hybridize to these sequences can be used to detect and/or to identify the corresponding HPV types according to the methods of the present invention.

Example 6: Broad-spectrum detection of HPV by amplification of a short PCR fragment using a mixture of 10 HPV primers

Introduction

The examples 1 and 2 describe the selection and optimization of a novel HPV PCR primerset. The selected primers from example 2, SGP1A, SGP1B, SGP2B-bio and SGP2D-bio, could be used for efficient HPV amplification. Additional broad spectrum primers were developed for a more sensitive HPV DNA PCR assay. The current example describes the use of a mixture of 10 primers for highly sensitive detection of human papillomaviruses.

Materials and Methods

From alignments of HPV L1 sequences as shown in figure 1, forward and reverse primers were selected for sensitive amplification of HPVs, see table 11. The primers were tested on plasmids containing HPV genotypes 6, 13, 16, 18, 26, 34, 35, 39, 40, 42, 43, 51, 52, 53, 54, 55, 68, 69, 70, 74. These HPV plasmids were provided by Dr. E-M. de Villiers, Heidelberg, Germany (HPV genotypes 6, 13, 16, 18, 40, 51 and 53), Dr. R. Ostrow, Minneapolis, MN (HPV genotype 26), Dr. A. Lorincz, Silver Springs, MD (HPV genotypes 35 and 43), Dr. T. Matsukura, Tokyo, Japan (HPV genotype 69), and Dr. G. Orth, Paris, France (HPV genotypes 34, 39, 42, 52, 54, 55, 68, 70 and 74).

HPV DNA amplification was performed in a final reaction volume of 50 µl, containing 10 µl of small amounts of plasmid DNA, 10 mM Tris-HCl pH 9.0, 50 mM KCl, 2.5 mM $MgCl_2$, 0.1% Triton X-100, 0.01% gelatin, 200 mM of each deoxynucleoside triphosphate, 15 pmol of each forward (SGP1A-1D) and 15 pmol of different reverse primers, and 1.5 U of AmpliTaq gold (Perkin Elmer, Branchburg, New Jersey, USA). The PCR conditions were as follows: preheating for 9 min 94°C was followed by 40 cycles of 30 seconds 94°C, 45 seconds at 50°C or 52°C or 55°C and 45 seconds at 72°C, and a final

extension of 5 min at 72°C. PCR-products were analyzed on a 3% TBE agarose gel.

Results

Developed were 14 broad spectrum primers, 4 sense (SGP1A, SGP1B, SGP1C, SGP1D) and 10 antisense (SGP2B-bio, SGP2D-bio, SGP2H-bio, SGP2I-bio, SGP2J-bio, SGP2K-bio, SGP2L-bio, SGP2M-bio, SGP2N-bio, SGP2P-bio), respectively. See table 11 for sequences and positions. For selection of sensitive PCR primers, plasmid DNA from HPV genotypes 6, 13, 16, 18, 26, 34, 35, 39, 40, 42, 43, 51, 52, 53, 54, 55, 68, 69, 70 and 74 were used as target. PCR experiments were performed with the 4 sense primers (SGP1A, SGP1B, SGP1C, SGP1D) in combination with one or more reverse primers at different annealing temperatures, using low amounts of HPV plasmid DNA. The reverse primers SGP2H-bio, SGP2I-bio, SGP2L-bio and SGP2N-bio appeared to have no added value compared to a mixture of the remaining 6 reverse primers (SGP2B-bio, SGP2D-bio, SGP2J-bio, SGP2K-bio, SGP2M-bio and SGP2P-bio) as listed in table 11.

Although the sequences of the 10 primers, 4 sense (SGP1A-1D) and 6 antisense (SGP2B-bio, SGP2D-bio, SGP2J-bio, SGP2K-bio, SGP2M-bio and SGP2P-bio) showed minor mismatches compared to known HPV genotypes (figure 1), still low amounts of HPV DNA could efficiently be amplified.

Discussion

A mixture of 10 primers was developed for broad-spectrum detection of HPV. Despite minor mismatches between primer and target sequences of known HPVs, the 10 selected primers were succesfull to detect various HPV genotypes at low levels. Therefore, this mixture of 10 primers can be used for sensitive broad-spectrum detection of HPV.

Example 7: A Line Probe Assay for Rapid Detection and Simultaneous Identification of 25 Different HPV Genotypes

Introduction

Example 4 describes the development of the HPV INNO-LiPA genotyping assay for

simple detection and identification of HPV genotypes. This example describes an HPV INNO-LiPA genotyping assay for simultaneous detection and identification of 25 types. After universal HPV amplification, synthesized amplimers can be detected and identified by hybridization to type-specific probes that are applied on a LiPA strip.

Materials and Methods

Based on the inner primer sequence of 22 bp which is located between the regions B and C (figure 9), several type-specific probes were proposed and tested for specificity reasons. The selected probes are listed in tables 7 and 12. Plasmids containing HPV sequences of different genotypes were used as target for broad-spectrum amplification (see examples 4 and 6). LiPA experiments were performed as described in example 4 using the Auto-LiPA system.

Results

Amplimers obtained from well defined plasmids containing HPV sequences of various genotypes were used in LiPA experiments in order to determine the specificity of the selected probes (tables 7 and 12). Subsequently, 25 HPV type-specific probes and another 3 probes were selected for simultaneous identification of 25 different HPV genotypes. The outline of the HPV-LiPA is shown in figure 10 and typical LiPA patterns are shown in figure 11.

In most cases the probe name is directly linked to the HPV type (e.g. a purple color on probe lane 16 means hybridization of an amplimer derived from HPV type 16). The probes c31, c56 and c68 are secundairy probes. These probes are of interest when there is a positive hybridization with the probe line just above (31/40/58 or 56/74 or 68/45). These 'c' probes were developed for exclusion of type 40, 58, 74, and 45. Those types are also identified by positive hybridization. The 'c' probes c31, c56 and c68 will also react with other types. Amplimers from type 33 and 54 will give a positive reaction with probe c31. Similarly, the amplimer from type 58 hybridizes with c56. Therefore, amplimers of type 58 will give three bands on a LiPA strip (positive on: 31/40/58 and c56 and 58). Probe c68 is also reactive with amplimers from type 18 and 39. HPV type 6 is identified by hybridization to the probes 6. HPV type 74 is identified by the probes 56/74 and 74. A sample contains type 54 when probe c31 is positive while probes 31/40/58, 33, 40, and 58 are negative.

Discussion

The described HPV LiPA genotyping assay detects and identifies simultaneously the HPV genotypes 6, 11, 16, 18, 31, 33, 34, 35, 39, 40, 42, 43, 44, 45, 51, 52, 53, 54, 56, 58, 59, 66, 68, 70, and 74. These genotypes can be recognized after universal PCR using the novel developed primerset as described in this patent and the MY11/09 primerset which is discussed in example 4. This typing assay can still be extended with type-specific probes for recognition of other HPV genotypes.

In summary, the novel PCR system for highly sensitive detection of HPV DNA in diverse clinical materials followed by a HPV LiPA typing experiment could be a usefull tool to improve the molecular diagnosis and epidemiology of HPV infections.

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CLAIMS

1. Method for detection and/or identification of HPV present in a biological sample, comprising the following steps:

(i) amplification of a polynucleic acid fragment of HPV by use of:

- a 5'-primer specifically hybridizing to the A region or B region of the genome of at least one HPV type, said A region or B region being indicated in figure 1, and,
- a 3'-primer specifically hybridizing to the C region of the genome of at least one HPV type, said C region being indicated in figure 1;

(ii) hybridizing the amplified fragments from step (i) with at least one probe capable of specific hybridization with the D region of at least one HPV type, said D region being indicated in figure 1.

2. Method according to claim 1, characterized further in that:

- the 3'-end of said 5'-primer specifically hybridizing to the A region of the genome of at least one HPV type, is situated at position 6572 of the genome of HPV 16, or at the corresponding position of any other HPV genome, as indicated in figure 1, and/or,
- the 3'-end of said 5'-primer specifically hybridizing to the B region of the genome of at least one HPV type, is situated at position 6601 of the genome of HPV 16, or at the corresponding position of any other HPV genome, as indicated in figure 1, and/or,
- the 3'-end of said 3'-primer specifically hybridizing to the C region of the genome of at least one HPV type, is situated at position 6624 of the genome of HPV 16, or at the corresponding position of any other HPV genome, as indicated in figure 1.

3. A method according to claim 2, characterized further in that:

- said 5'-primer specifically hybridizing to the A region is chosen from the following list:

SGP3 (SEQ ID NO 2), SGP3A (SEQ ID NO 3), SGP3B (SEQ ID NO 4), SGP3C (SEQ ID NO 10), SGP3D (SEQ ID NO 11), SGP3E (SEQ ID NO 12), SGP3F (SEQ ID NO 13), SGP3G (SEQ ID NO 14), and/or,

- said 5'-primer specifically hybridizing to the B region is chosen from the following list:

SGP1 (SEQ ID NO 6), SGP1A (SEQ ID NO 15), SGP1B (SEQ ID NO16), SGP1C

(SEQ ID NO 17), SGP1D (SEQ ID NO 18), and/or,

- said 3'-primer specifically hybridizing to the C region is chosen from the following list:

SGP2 (SEQ ID NO 9), SGP2A (SEQ ID NO 8), SGP2B (SEQ ID NO 19), SGP2C (SEQ ID NO 20), SGP2D (SEQ ID NO 21), SGP2E (SEQ ID NO 22), SGP2F (SEQ ID NO 23), SGP2H (SEQ ID NO 98), SGP2I (SEQ ID NO 154), SGP2J (SEQ ID NO 155), SGP2K (SEQ ID NO 156), SGP2L (SEQ ID NO 157), SGP2M (SEQ ID NO 158), SGP2N (SEQ ID NO 159), SGP2P (SEQ ID NO 160).

4. Method according to any of claims 1 to 3, characterized further in that said probe mentioned in step (ii) is capable of specific hybridization with the D region of the genome of only one HPV type, and thus enables specific identification of this HPV type, when this type is present in a biological sample.

5. Method according to any of claims 1 to 3, characterized further in that said probe mentioned in step (ii) is capable of specific hybridization with the D region of more than one HPV type, and thus enables detection of any of said more than one HPV type, when any of said types is present in a biological sample.

6. Method according to claim 4, characterized further in that said probe capable of specific hybridization with the D region of the genome of only one HPV type, more particularly hybridizes to the E region, with said E region being a subregion of the D region, as indicated in figure 1.

7. Method according to claim 4, characterized further in that said probe capable of specific hybridization with the D region of the genome of only one HPV type, more particularly specifically hybridizes to the 22 bp region situated between the B region and the C region, as indicated in figure 1.

8. Method according to claim 7, characterized further in that said probe specifically hybridizing to said 22 bp region of only one HPV type is chosen from the following list:

HPV6 Pr1, HPV6 Pr2, HPV6 Pr3, HPV6 Pr4, HPV6 Pr5, HPV11 Pr1, HPV11 Pr2,

HPV11 Pr3, HPV11 Pr4, HPV11 Pr5, HPV16 Pr1, HPV16 Pr2, HPV16 Pr3, HPV16 Pr4, HPV16 Pr5, HPV18 Pr1, HPV18 Pr2, HPV18 Pr3, HPV18 Pr4, HPV18 Pr5, HPV31 Pr1, HPV31 Pr2, HPV31 Pr3, HPV31 Pr4, HPV31 Pr5, HPV31 Pr21, HPV31 Pr22, HPV31 Pr23, HPV31 Pr24, HPV31 Pr25, HPV31 Pr26, HPV31 Pr31, HPV31 Pr32, HPV33 Pr1, HPV33 Pr2, HPV33 Pr3, HPV33 Pr4, HPV33 Pr5, HPV33 Pr21, HPV33 Pr22, HPV33 Pr23, HPV33 Pr24, HPV33 Pr25, HPV33 Pr26, HPV40 Pr1, HPV45 Pr1 (= SGPP68), HPV45 Pr2, HPV45 Pr3, HPV45 Pr4, HPV45 Pr5, HPV45 Pr11, HPV45 Pr12, HPV45 Pr13, HPV52 Pr1, HPV52 Pr2, HPV52 Pr3, HPV52 Pr4, HPV52 Pr5 HPV52 Pr6, HPV56 Pr1, HPV56 Pr2, HPV56 Pr3, HPV56 Pr11, HPV56 Pr12, HPV58 Pr1, HPV58 Pr2, HPV58 Pr3, HPV58 Pr4 (SEQ ID NOs 24 to 91), and,

SGPP35, SGPP39, SGPP51 (= HPV51 Pr1), SGPP54, SGPP59, SGPP66, SGPP70 (= HPV70 Pr1), SGPP13, SGPP34, SGPP42, SGPP43, SGPP44, SGPP53, SGPP55, SGPP69, SGPP61, SGPP62, SGPP64, SGPP67, SGPP74 (= HPV74 Pr13), MM4 (= HPVM4 Pr11), MM7, MM8 (SEQ ID NOs 92 to 115), and,

HPV18b Pr1, HPV18b Pr2, HPV31 Vs40-1, HPV31 Vs40-2, HPV31 Vs40-3, HPV34 Pr1, HPV35 Pr1, HPV35 Pr2, HPV35 Pr3, HPV39 Pr1, HPV42 Pr1, HPV42 Pr2, HPV43 Pr1, HPV43 Pr2, HPV43 Pr3, HPV44 Pr1, HPV44 Pr2, HPV44 Pr3, HPV44 Pr4, HPV51 Pr2, HPV53 Pr1, HPV54 Pr1, HPV54 Pr11, HPV54 Pr11as, HPV54 Pr12, HPV55 Pr1, HPV55 Pr11, HPV55 Pr12, HPV55 Pr13, HPV56 Vs74-1, HPV59 Pr1, HPV59 Pr11, HPV59 Pr12, HPV59 Pr13, HPV66 Pr1, HPV67 Pr1, HPV67 Pr11, HPV67 Pr12, HPV67 Pr13, HPV67 Pr21, HPV67 Pr22, HPV67 Pr23, HPV68 Pr1, HPV68 Pr2, HPV68 Pr3, HPV68 Vs45-1, HPV68 Vs45-2, HPV70 Pr1, HPV70 Pr12, HPV70 Pr13, HPV74 Pr1, HPV74 Pr11, HPV74 Pr12, HPV74 Pr2, HPV74 Pr3, HPVM4 Pr1, HPVM4 Pr12, HPVM4 Pr21, HPVM4 Pr22 (SEQ ID NOs 161 to 219).

9. Method according to claim 5, characterized further in that said probe capable of specific hybridization with the D region of the genome of more than one HPV type, more particularly hybridizes to the E region, with said E region being a subregion of the D region, as indicated in figure 1.

10. Method according to claim 9, characterized further in that said probe specifically

hybridizing to said E region of more than one HPV type, is chosen from the following list:

HPVuni1, HPVuni2, HPVuni3, HPVuni4, HPVuni5, HPVuni6, HPVuni7, HPVuni2L2, HPVuni2L3, HPVuni2L4, HPVuni2L5, HPVuni2L6, HPVuni2L7, HPVuni4L1, HPVuni4L2, HPVuni4L3, HPVuni4L4, HPVuni4L5, HPVuni4L6 (SEQ ID NOs 116 to 134), and,

HPVuni1A, HPVuni1B, HPVuni1C, HPVuni2A, HPVuni3A (SEQ ID NOs 220 to 224), and,

HPV G1, HPV G1A1, HPV G1A2, HPV G1A3, HPV G1A4, HPV G2, HPV G3, HPV G4, HPV G5, HPV G6, HPV R1, HPV R10, HPV R11, HPV R2, HPV R3, HPV R4, HPV R5, HPV R6, HPV R7, HPV R8, HPV R9 (SEQ ID NOs 225 to 245).

11. A primer as defined in any of claims 1 to 3, for use in the detection and/or identification of HPV present in a biological sample.

12. A primer combination consisting of a 5'-primer as defined in any of claims 1 to 3 and of a 3'-primer as defined in any of claims 1 to 3, for use in the detection and/or identification of HPV present in a biological sample.

13. A probe as defined in any of claims 1 and 4 to 10, for use in the detection and/or identification of HPV present in a biological sample.

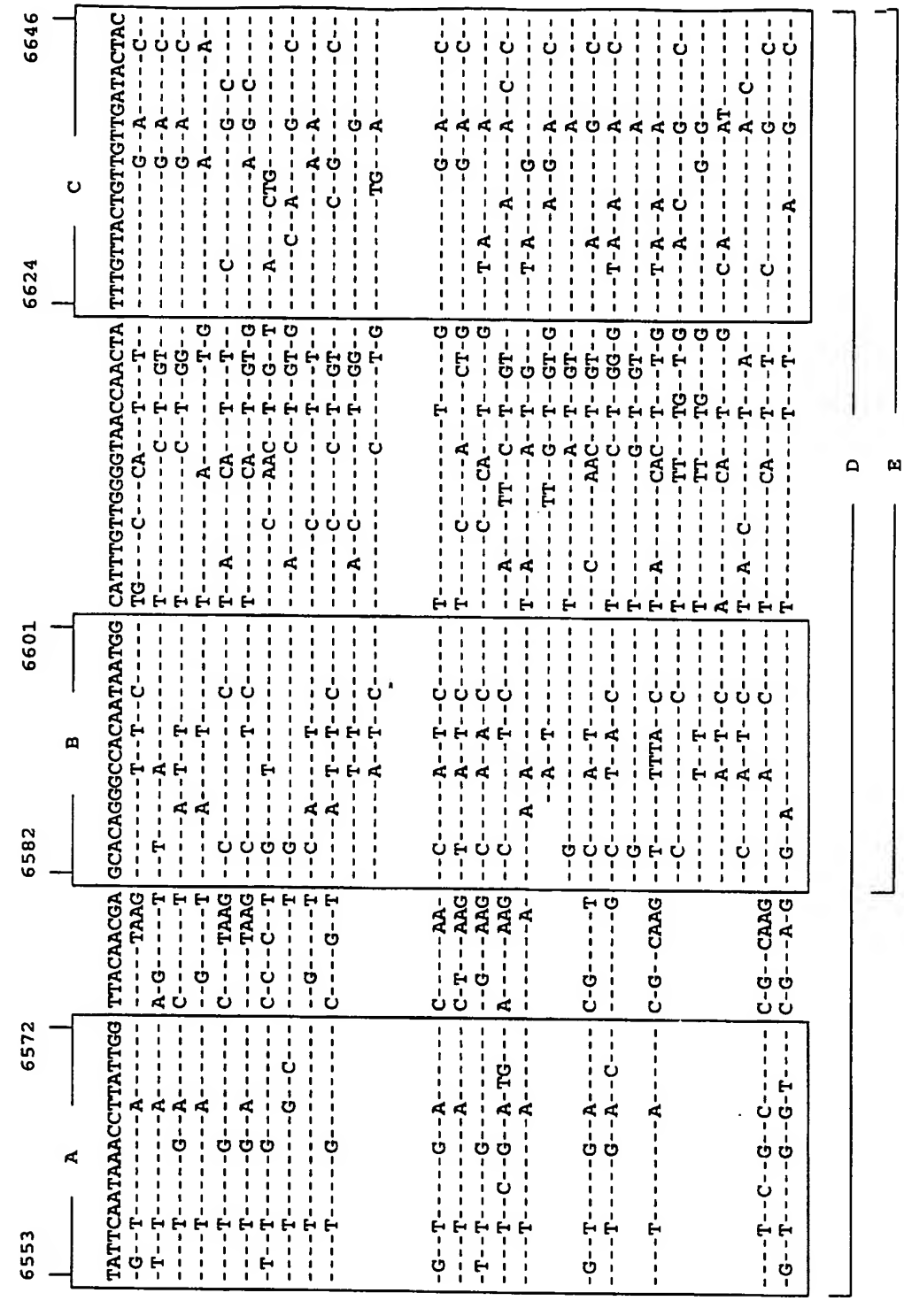
14. A diagnostic kit for detection and/or identification of HPV, possibly present in a biological sample, comprising the following components:

(i) at least one suitable primer, with said primers being defined in any of claims 1 to 3;

(ii) at least one suitable probe, with said probes being defined in any of claims 1 and 4 to 10.

15. An isolated HPV polynucleic acid, defined by SEQ ID NO 135 to 153, or any fragment thereof, that can be used as a primer or as a probe in a method for detection and/or identification of HPV present in a sample.

Figure 1: Alignment of HPV sequences



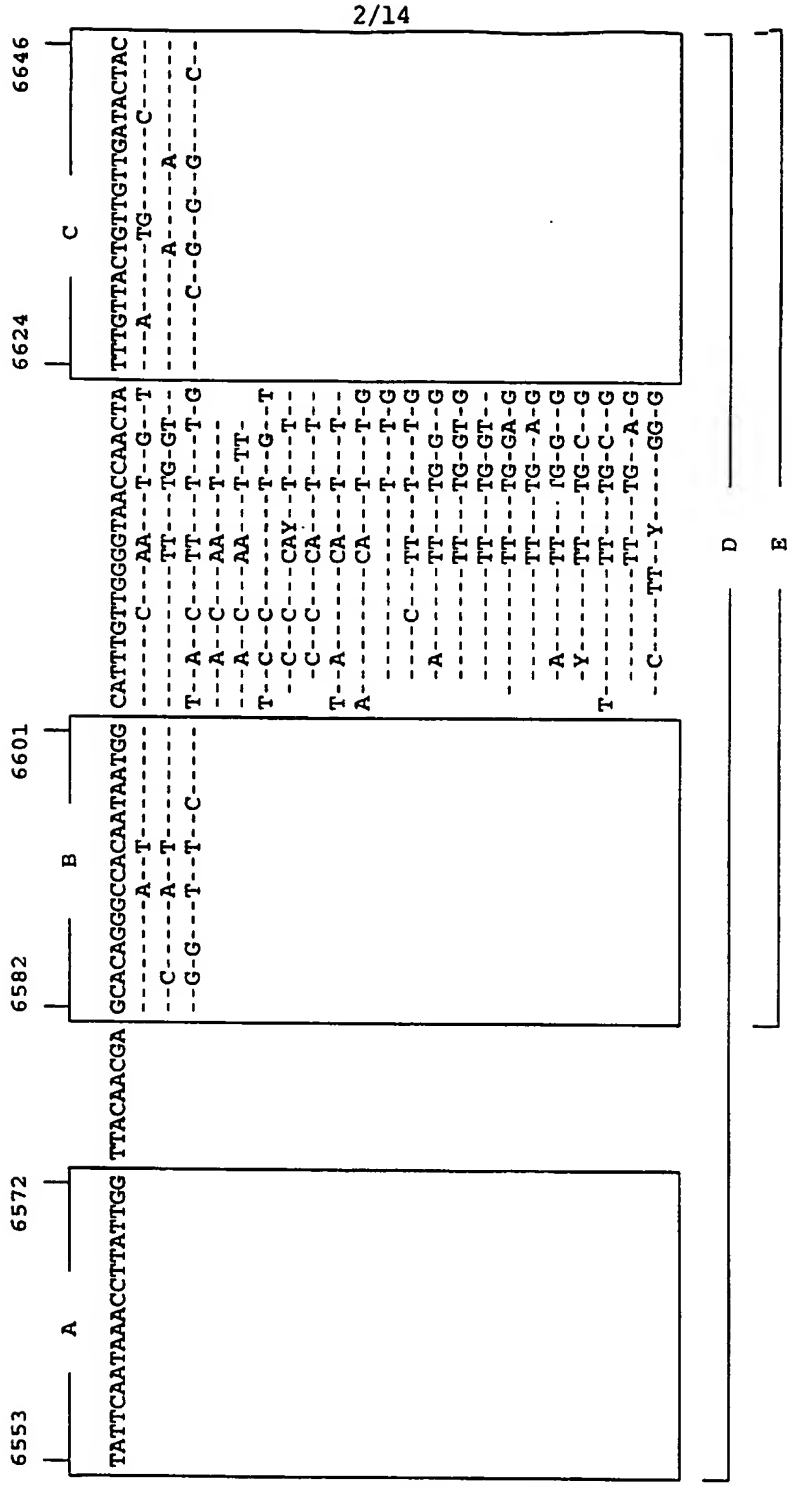


Figure 1 (continued): Alignment of HPV sequences

Figure 2: Outline of the HPV DNA genome

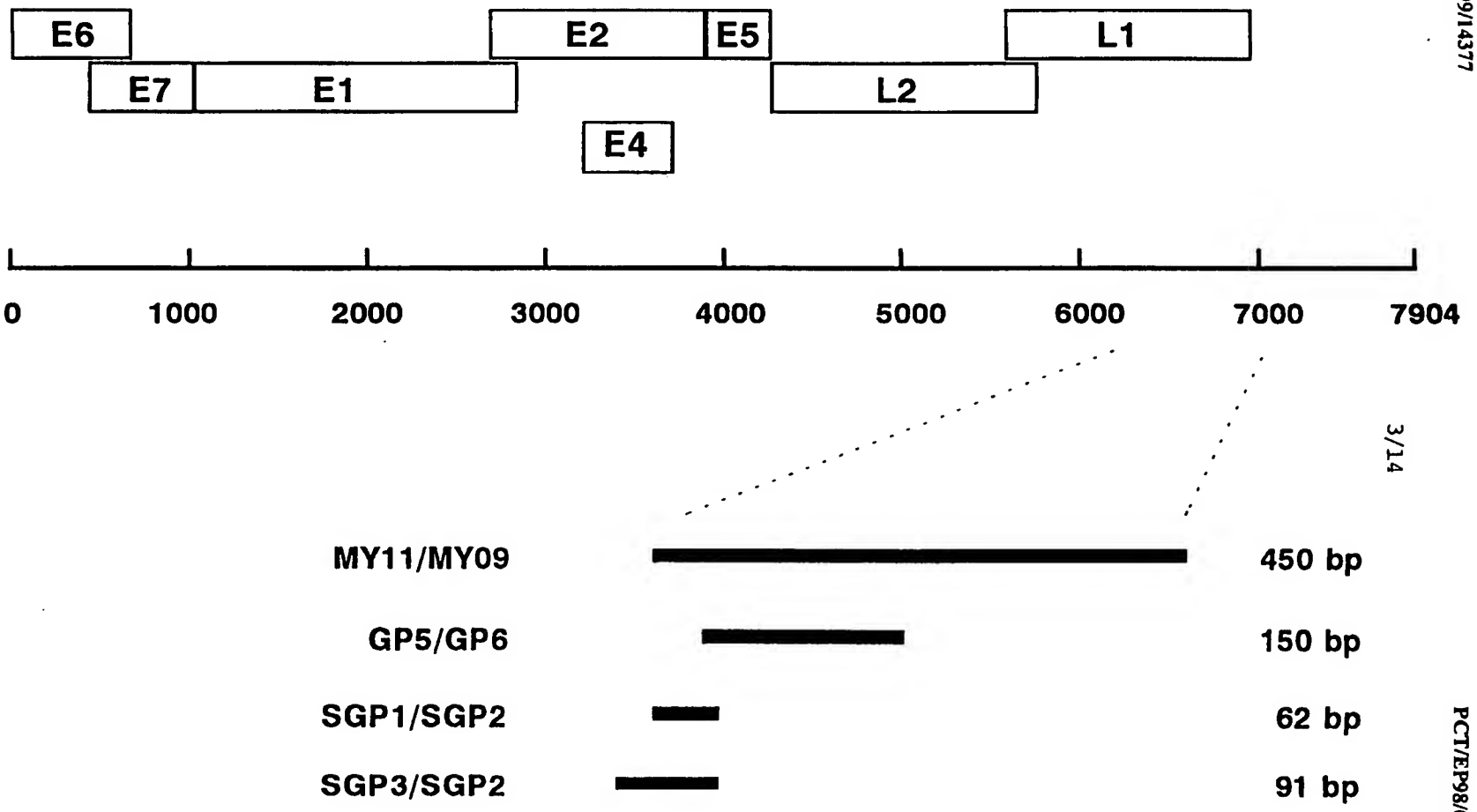


Figure 3: Phylogenetic tree of HPV sequences in the My11/09 region

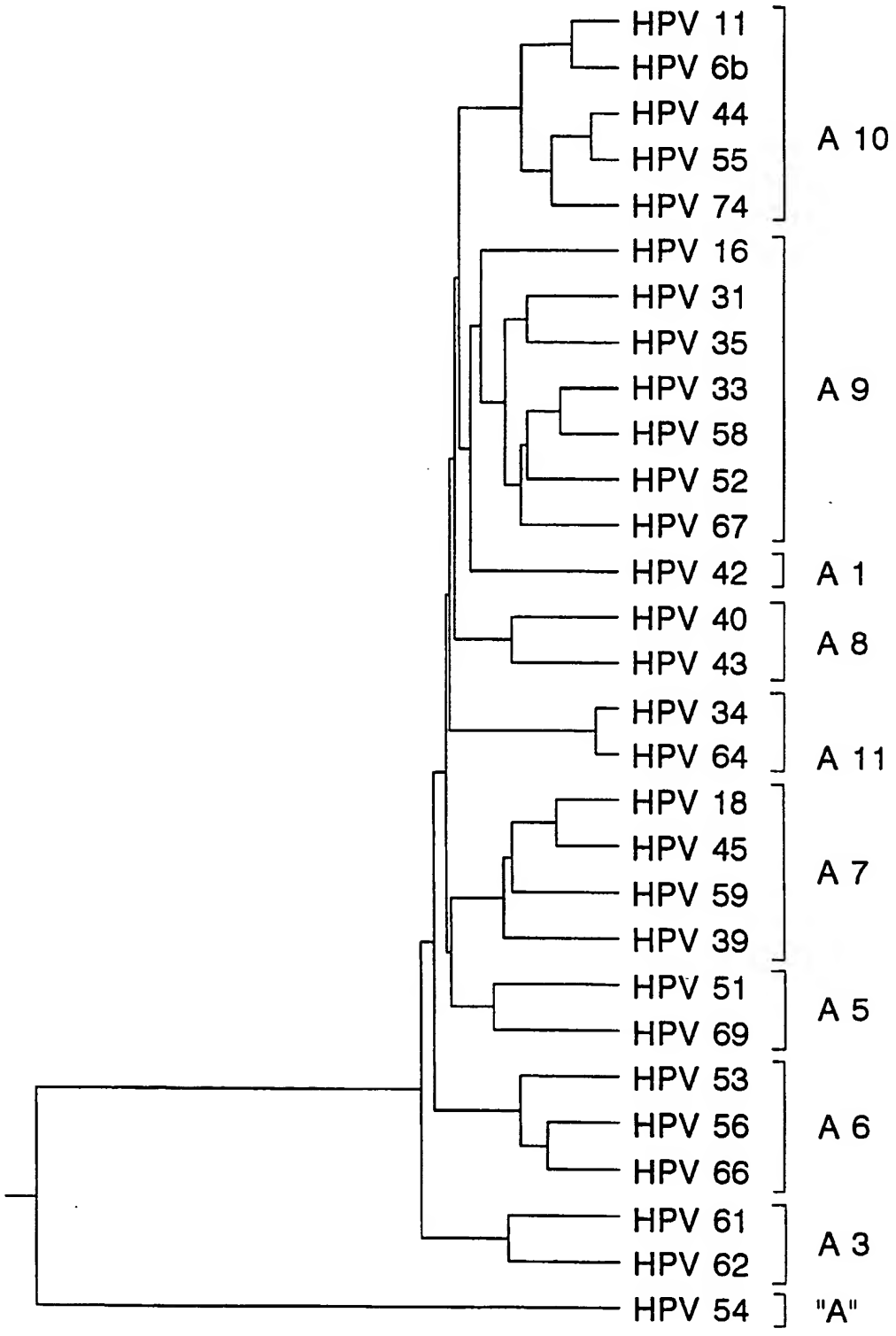


Figure 4: Phylogenetic tree of HPV sequences between the B and C regions

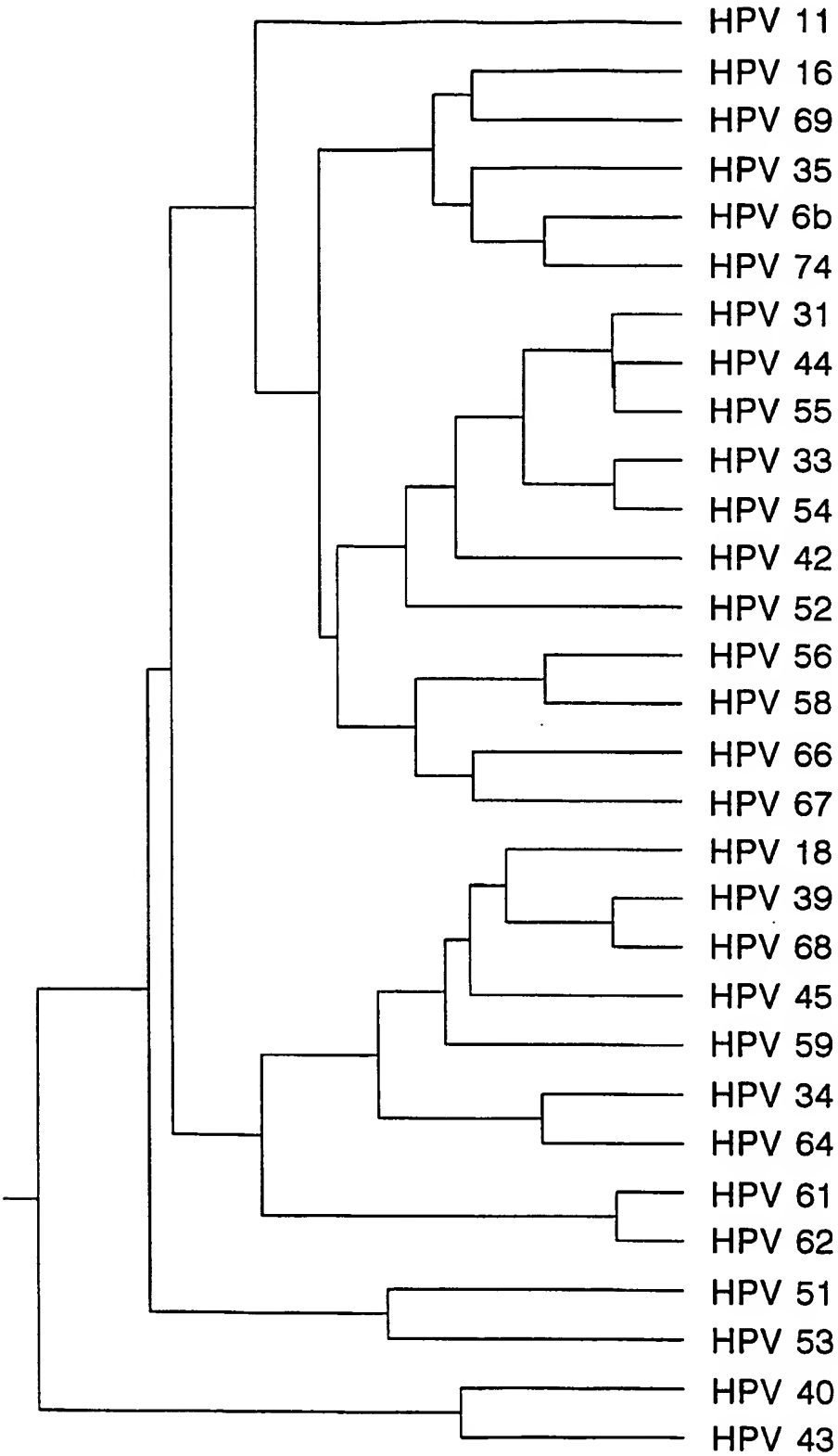


Figure 5: Phylogenetic tree of HPV sequences between the A and C regions

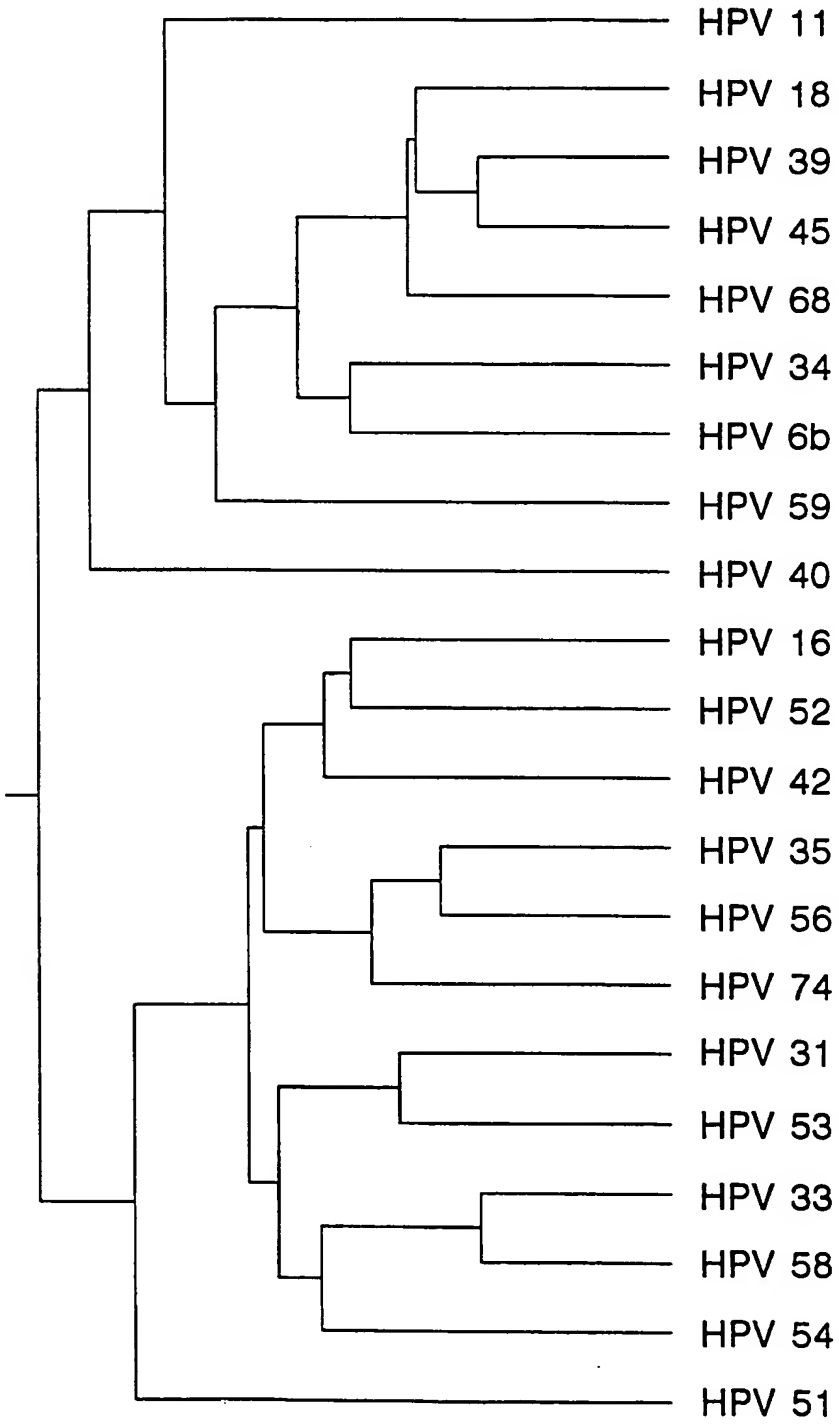
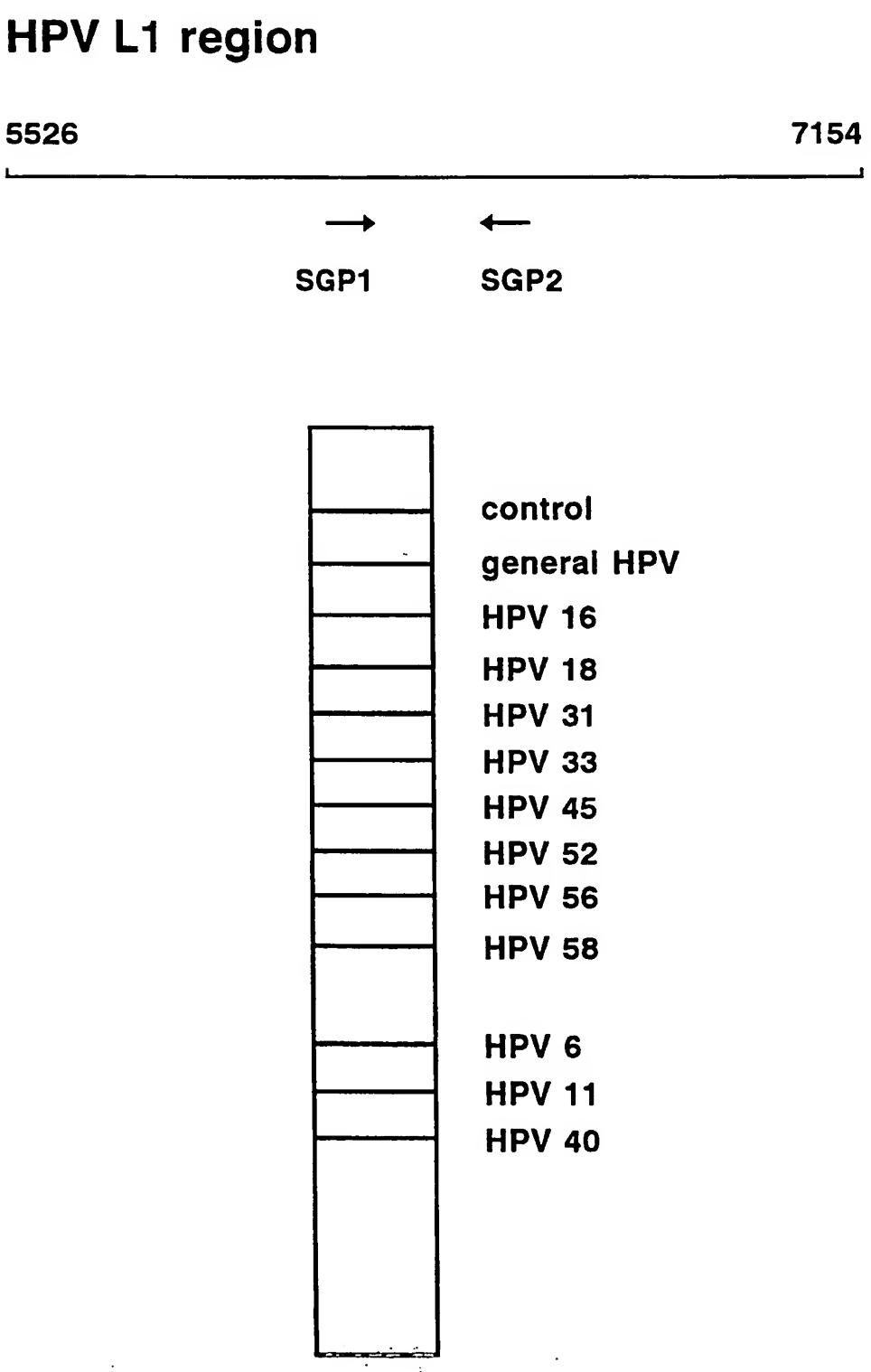


Figure 6: Outline of a HPV LiPA



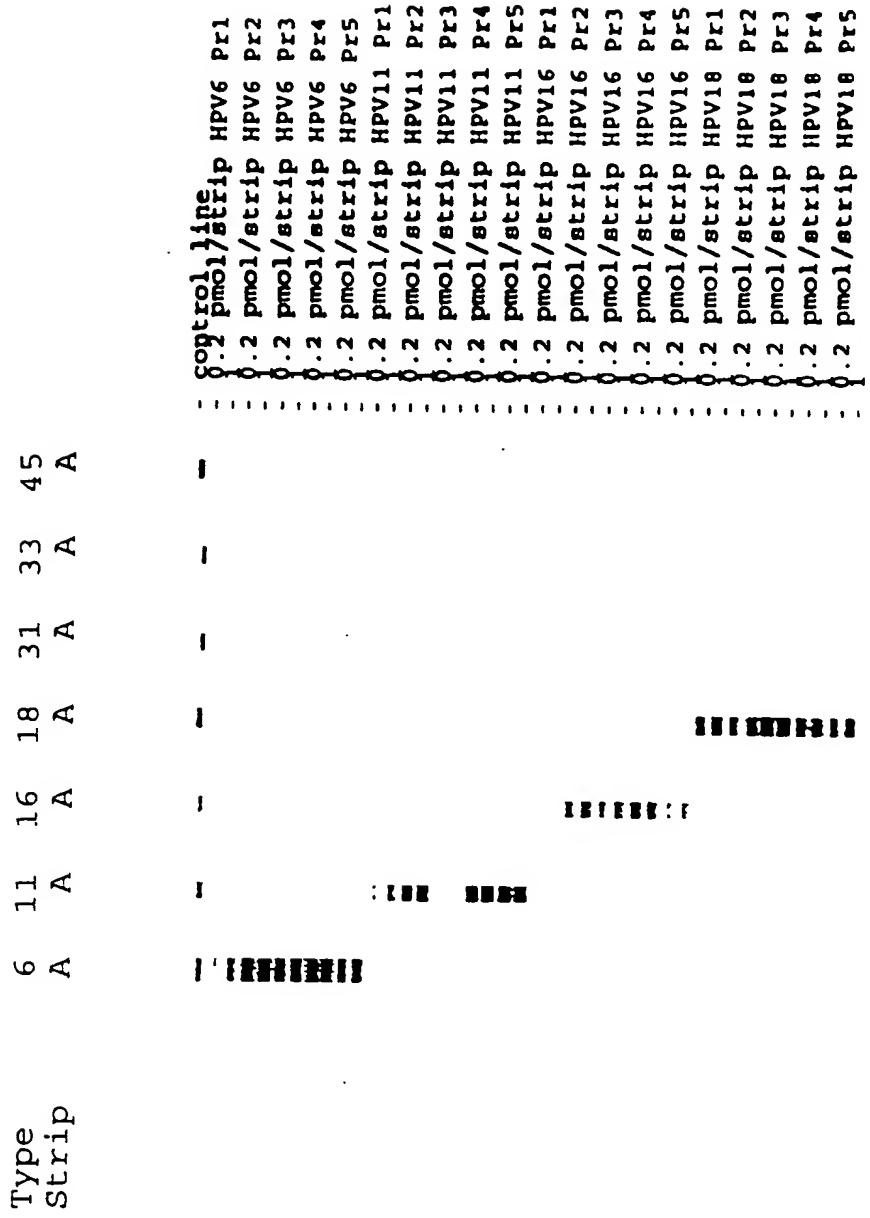

control line
0.2 pmol/strip HPV6 Pr1
0.2 pmol/strip HPV6 Pr2
0.2 pmol/strip HPV6 Pr3
0.2 pmol/strip HPV6 Pr4
0.2 pmol/strip HPV6 Pr5
0.2 pmol/strip HPV11 Pr1
0.2 pmol/strip HPV11 Pr2
0.2 pmol/strip HPV11 Pr3
0.2 pmol/strip HPV11 Pr4
0.2 pmol/strip HPV11 Pr5
0.2 pmol/strip HPV16 Pr1
0.2 pmol/strip HPV16 Pr2
0.2 pmol/strip HPV16 Pr3
0.2 pmol/strip HPV16 Pr4
0.2 pmol/strip HPV16 Pr5
0.2 pmol/strip HPV18 Pr1
0.2 pmol/strip HPV18 Pr2
0.2 pmol/strip HPV18 Pr3
0.2 pmol/strip HPV18 Pr4
0.2 pmol/strip HPV18 Pr5
6 11 16 18 31 33 45
A A A A A A A
Type
Strip

Figure 7A

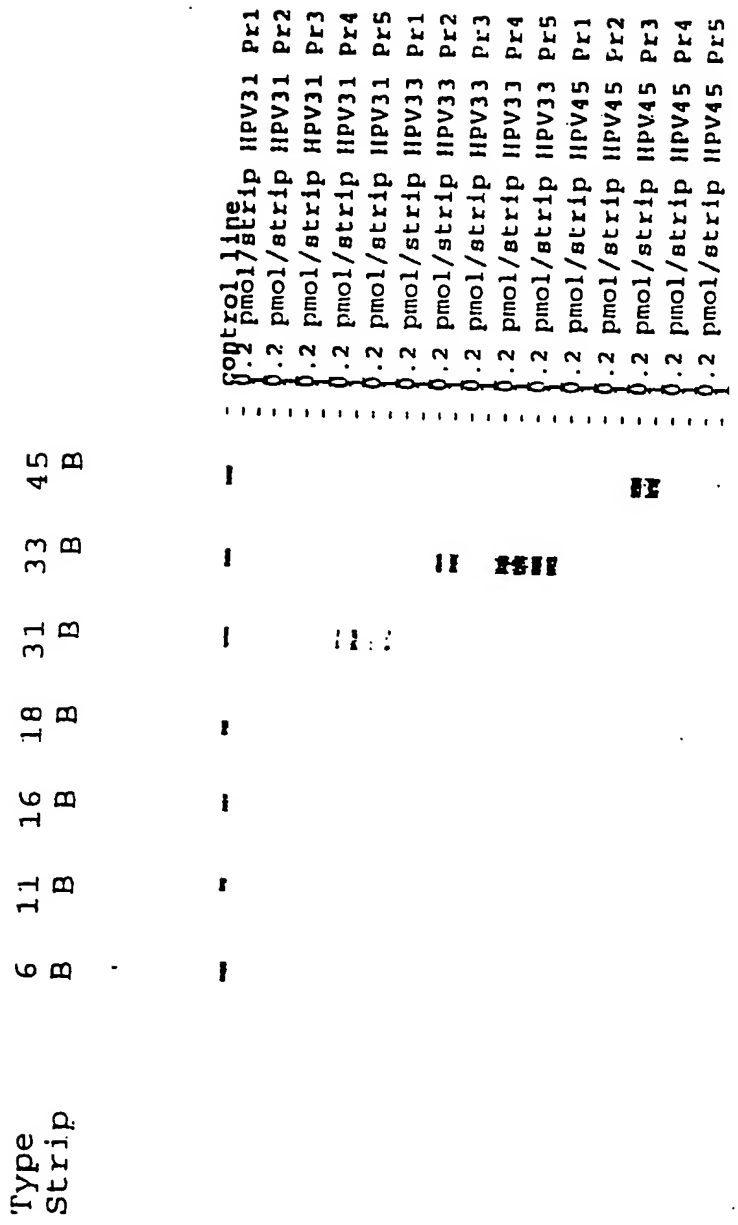
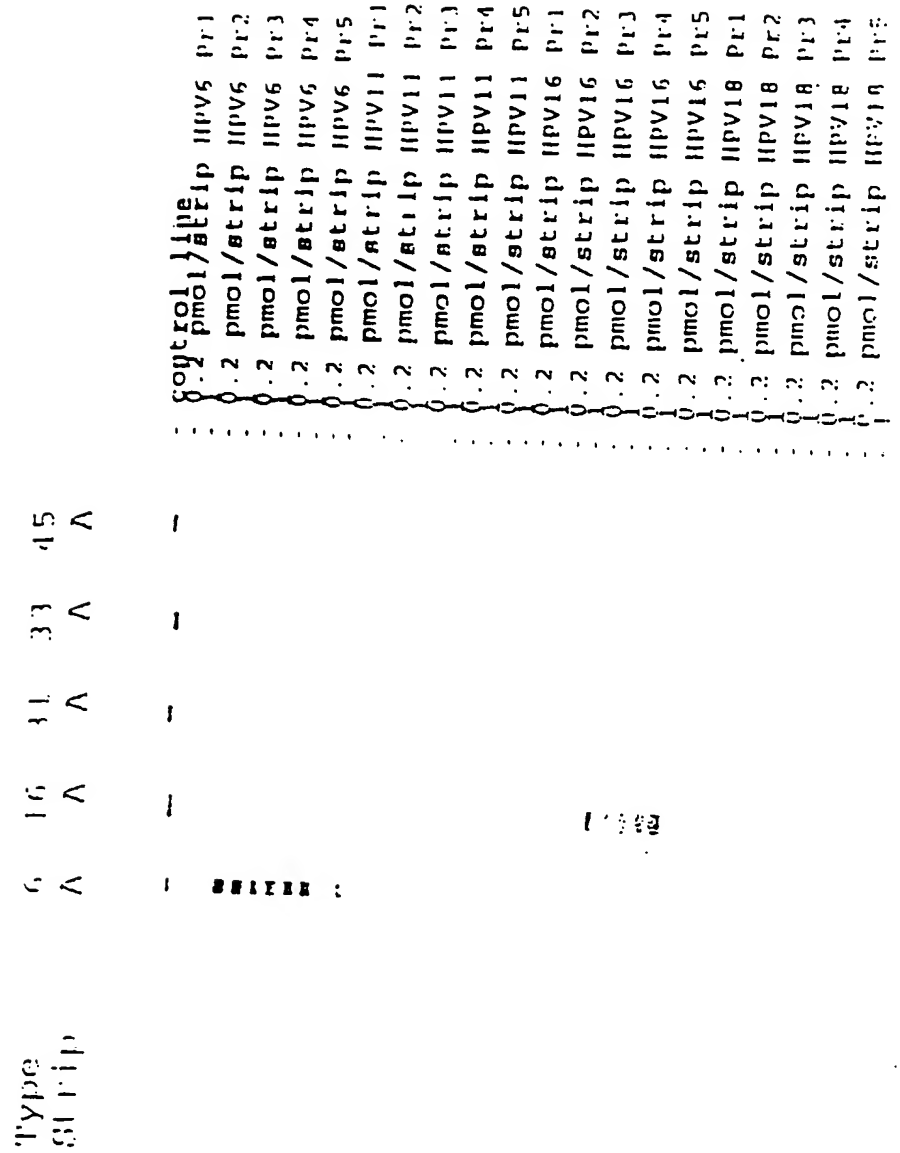

Type
Strip
6 11 16 18 31 33 45
B B B B B B B
Control line
0.2 pmol/strip HPV31 Pr1
0.2 pmol/strip HPV31 Pr2
0.2 pmol/strip HPV31 Pr3
0.2 pmol/strip HPV31 Pr4
0.2 pmol/strip HPV31 Pr5
0.2 pmol/strip HPV33 Pr1
0.2 pmol/strip HPV33 Pr2
0.2 pmol/strip HPV33 Pr3
0.2 pmol/strip HPV33 Pr4
0.2 pmol/strip HPV33 Pr5
0.2 pmol/strip HPV45 Pr1
0.2 pmol/strip HPV45 Pr2
0.2 pmol/strip HPV45 Pr3
0.2 pmol/strip HPV45 Pr4
0.2 pmol/strip HPV45 Pr5

Figure 7B


Control line
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.2 pmol/strip HPV6 Pr2
.2 pmol/strip HPV6 Pr3
.2 pmol/strip HPV6 Pr4
.2 pmol/strip HPV6 Pr5
.2 pmol/strip HPV11 Pr1
.2 pmol/strip HPV11 Pr2
.2 pmol/strip HPV11 Pr3
.2 pmol/strip HPV11 Pr4
.2 pmol/strip HPV11 Pr5
.2 pmol/strip HPV16 Pr1
.2 pmol/strip HPV16 Pr2
.2 pmol/strip HPV16 Pr3
.2 pmol/strip HPV16 Pr4
.2 pmol/strip HPV16 Pr5
.2 pmol/strip HPV18 Pr1
.2 pmol/strip HPV18 Pr2
.2 pmol/strip HPV18 Pr3
.2 pmol/strip HPV18 Pr4
.2 pmol/strip HPV18 Pr5
Type
Strip

Figure 8A

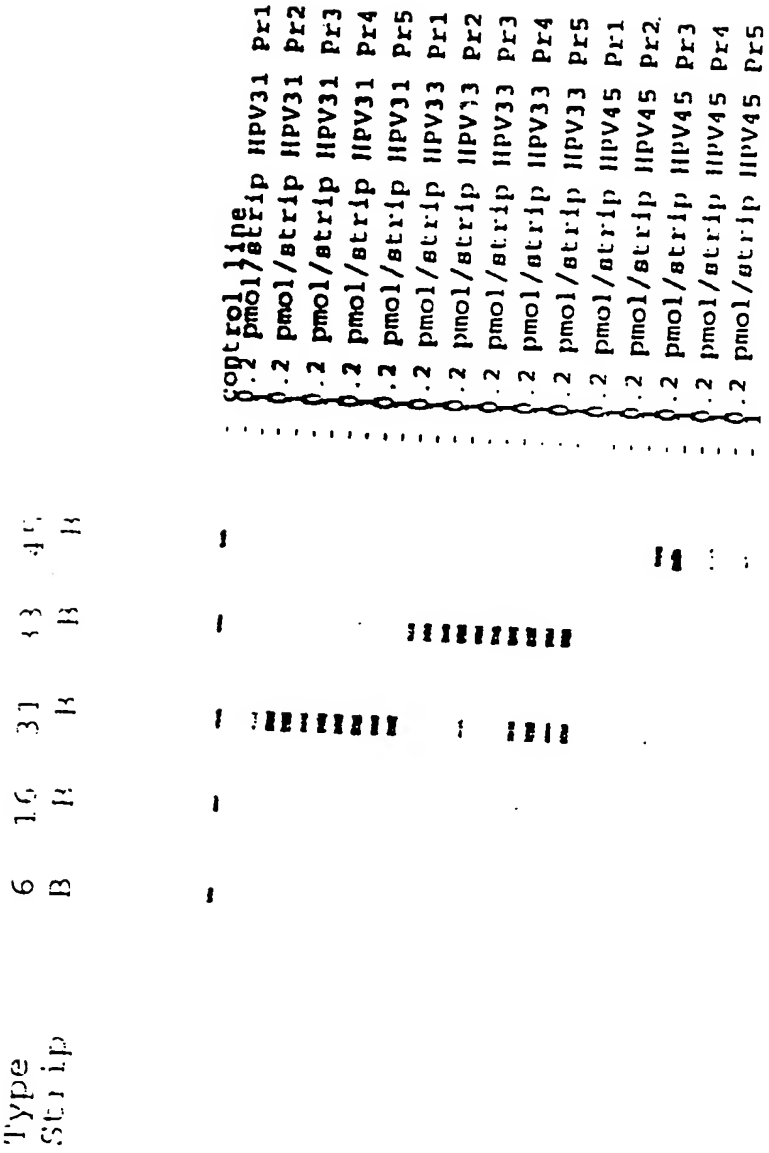

Type
Strip
6
11
16
31
33
45
Control line
0.2 pmol/strip HPV31 Pr1
0.2 pmol/strip HPV31 Pr2
0.2 pmol/strip HPV31 Pr3
0.2 pmol/strip HPV31 Pr4
0.2 pmol/strip HPV31 Pr5
0.2 pmol/strip HPV33 Pr1
0.2 pmol/strip HPV33 Pr2
0.2 pmol/strip HPV33 Pr3
0.2 pmol/strip HPV33 Pr4
0.2 pmol/strip HPV33 Pr5
0.2 pmol/strip HPV45 Pr1
0.2 pmol/strip HPV45 Pr2
0.2 pmol/strip HPV45 Pr3
0.2 pmol/strip HPV45 Pr4
0.2 pmol/strip HPV45 Pr5

Figure 8B

Figure 9: Nucleotide sequence alignments of 39 HPV genotypes

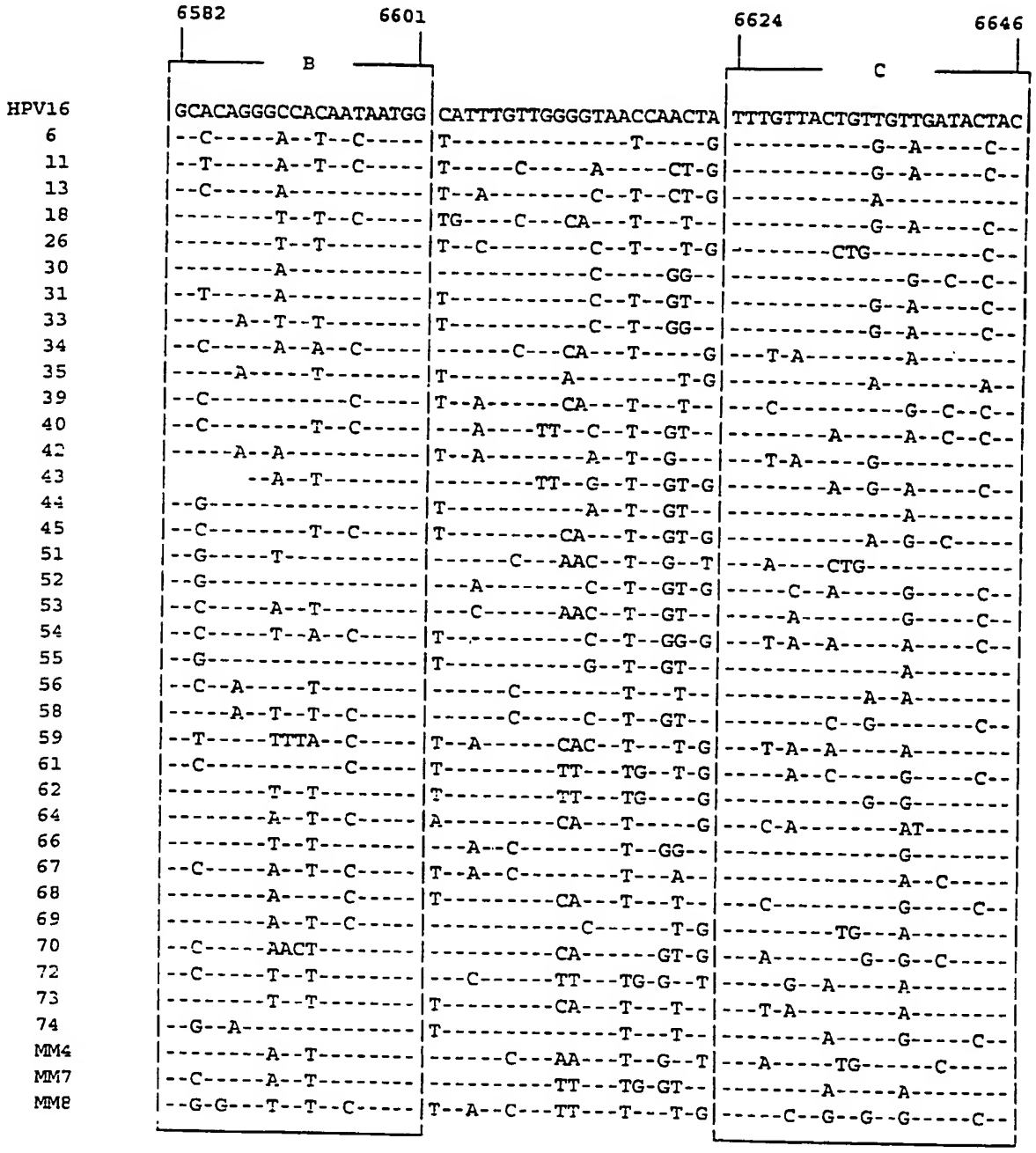
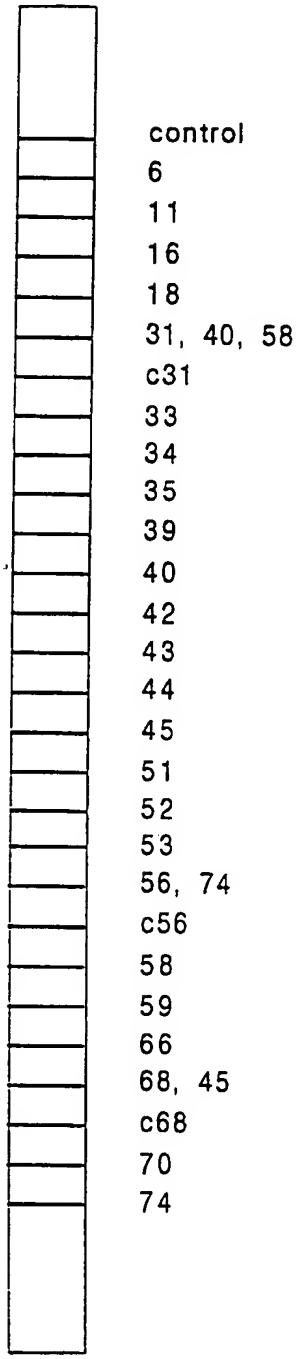


Figure 10: Outline HPV-LiPA for identification of 25 types



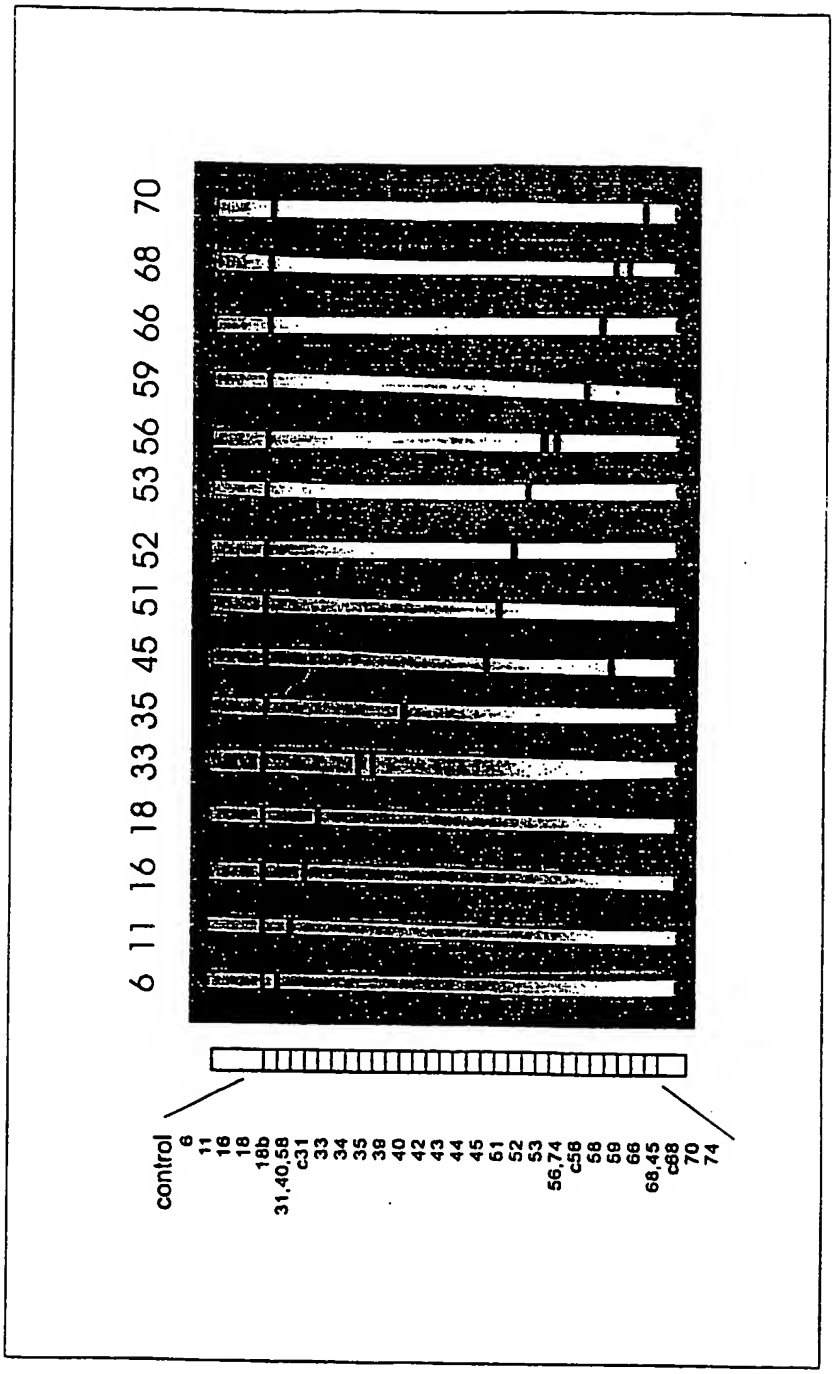


Figure 11: Typical HPV LiPA patterns

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(57) Abstract

The present invention relates to a method for detection and/or identification of HPV present in a biological sample, comprising the steps of amplification of HPV polynucleic acids and of hybridization of said amplified polynucleic acids to a number of probes. By means of PCR, a short fragment of the L1 gene of HPV is amplified. The amplimers are then contacted with probes that specifically hybridize to said short fragment of the L1 gene of either one or more than one HPV type. A preferred format is the reverse hybridization technique, more particularly the LiPA technique. The invention also relates to primers and probes to be used in a method of detection and/or identification of HPV and to a diagnostic kit to perform said method.

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